RESULT 9
LOCUS   BF439382/c
LOCUS   BF439382   696 bp   mRNA   linear   EST 30-MAR-2001
DEFINITION nab63g06.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
            IMAGE:3272627 3' similar to SW:GP39_HUMAN O43194 PUTATIVE G
            PROTEIN-COUPLED RECEPTOR GPR39. ;, mRNA sequence.
ACCESSION   BF439382
VERSION   BF439382.1 GI:11451899
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 696)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40UP from Gibco
            High quality sequence stop: 459.
FEATURES   Location/Qualifiers
     source   1..696
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3272627"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Equal amounts of plasmid DNA from five normalized
                     libraries were mixed, and ss circles were made in vitro.
                     Following HAP purification, this DNA was used as tracer in
                     a subtractive hybridization reaction. The driver was
                     PCR-amplified cDNAs from pools of 5,000 clones made from
                     the same 5 libraries. The pools consisted of the following
                     libraries and cloneIDs: Soares NHSF pool 1:
                     309384-310919, 323208-325895 Soares Nb2HP pool 1:
                     145032-147335, 147720-148103, 148872-149255, 15002 -
                     150407, 151176-152327 Soares Nb2HF8-9W pool 1:
                     758280-760583, 772104-774407 Soares NbHPA pool 1:
                     304776-306311, 320136-322823, 326280-326663 Soares NbHOT
                     pool 1: 723720-726407, 739080-740999 Subtraction by Bento
                     Soares and M. Fatima Bonaldo."
BASE COUNT   138 a   202 c   164 g   192 t
ORIGIN

Db   158 TTGGCCCCAGCCATGATCCTCCGAAATCTGGTTGTGGCATCCACGCATACGGCCAATGTCACA
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1620 ACAATCAGCCCTGGGCAGAGACACGAGCAGGAGGAGGAGACAGACAGAAAAAACACAGCA 1679
         |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   98 ACAATCAGCCCTGGGCAGAGACACGAGCAGGAGGGGAGAGACAGAGAGAAAAAGAAAAACACAGCA 39
Qy 1680 TGAGAACACAGTAAAT 1695
         ||||||||||||||||
Db   38 TGAGAACACAGTAAAT 23

Qy 1400 GCGGCGAGCACAGCACCTGCACGAACAACACCCCCGAGAAACTGCTGCGCGAGGAGGACACCGTGTACAG
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   483 GCGGCGAGCACAGCACCTGCACGAACAACACCCCGAGAAACTGCTGCGCGAGGAGGACACCGTGTACAG 424
Qy 1460 GAGCGGGTTGCATGACCGAGCTGAGGTAGAGAAAACGTTCTCCGAGAAGGGGAGGGAGGGAGGATCAT
         ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   423 GAGCGGGTTGATGACCGAGCTGAGGTAGAGAAAACGTTCTCCGAGAAGGGGAGGGAGGGAGGATCAT 364
Qy 1520 GTACGCCCGGAAGTAGGACCTCGTCCTGCTGCTTGGGTTGGGTTTGGGCCGCAGCCATGATCCT 1579
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   363 GTACGCCCGGAAGTAGGACCTCGTCCAGTGTCGTTGGGTTGGGTTTGGGCCGCAGCCATGATCCT 304
Qy 1580 CCGAATCTGGTTGGGCCATCCACGCATACGGCCAAGTCACAACAATCAGCCCCTGGGCAGAC 1639
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   303 CCGAATCTGGTTGGGCCATCCAGCATACGGCCAAGTCACAACAATCAGCCCCTGGGCAGAC 244
Qy 1640 ACGAGCACAGGAGAGGAGAGACAGAGAGAAAAAGAAAACACAGTAAAAT 1699
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   243 ACGAGCACAGGAGAGGAGAGACAGAGAGAAAAAGAAAACACAGTAAAAT 184
Qy 1700 AAAACCATAAAATATTTAGCCCCTCGTTCTGGCCAGGGAAATGGTACCAAT 1759
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   183 AAAACCATAAAATATTTACCCCTCGTTCTGGCCAGGGAAATGGTACCAAT 124
Qy 1760 TTTTCAGTGTTGGGACTTGACAGCTTCTTTTGCCACACGACAAGAGATTAACACTGTT 1819
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   123 TTTTCAGTGTTGGGACTTGACAGCTTCTTTTGCCACACGACAAGAGATTAACACTGTT 64
Qy 1820 TCAAACCCCGGGGAGAGTTGGCTGTGTGTTAAAGAAGAACCATTAAAATGCTTTTAGACAGTGTAA 1879
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   63 TCAAACCCGGGGAGAGTTGGCTGTGTTAAAGAAGAACCATTAAAATGCTTTTAGACAGTGTAA 4
Qy 1880 AAA 1882
         |||
Db   3 AAA 1

RESULT 10
LOCUS   BQ882838
LOCUS   BQ882838   948 bp   mRNA   linear   EST 16-AUG-2002
DEFINITION AGENCOURT_8627686 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:6291960
            5', mRNA sequence.
ACCESSION   BQ882838
VERSION   BQ882838.1 GI:22274846
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 948)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution Information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2492 row: k column: 01
            High quality sequence stop: 533.
FEATURES   Location/Qualifiers
     source   1..948
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6291960"
                     /clone_lib="NIH_MGC_43"
                     /tissue_type="normal pigmented retinal epithelium"
                     /lab_host="DH10B (phage-resistant)"

Query Match   29.1%;   Score 552; DB 12; Length 696;
Best Local Similarity   99.8%;   Pred. NO. 0;
Matches   602; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy 1280 TGCAGAGGACTGGCGCGCGGGACGGCGGGCGCCTGCACAAAGCGGCGGCGGCTGTC 1339
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   603 TGCAGAGGACTGGCGCCGCGGGACGGCGGGAGCAACGGCGCTTCTCGTGGTGTGGCGTGTGCTGGTC 544
Qy 1340 TGCAGAGGACTGGCGCCGCGGGACGCGAGAGCAACGGCGCTTCTCGTGGTGTGGCGTGCGGACGCGACAG 1399
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   543 GGTGGTGGGGAGGTGCGCATGTACCGCGACGCAGGCGGCGCTTCTCGTGGTGTGGCGTGCTGCAGCGACAG 484

```
                 /note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
                 EcoRI; cDNA made by oligo-dT priming. Directionally
                 cloned into EcoRI/XhoI sites using the following 5'
                 adaptor: GGCACGAG(G). Library constructed by Ling Hong
                 in the laboratory of Gerald M. Rubin (University of
                 California, Berkeley) using ZAP-cDNA synthesis kit
                 (Stratagene) and Superscript II RT (Life Technologies).
                 Note: this is a NIH_MGC Library."

BASE COUNT      183 a    288 c    286 g    190 t    1 others
ORIGIN

Query Match     100.0%;  Score 552;  DB 14;  Length 948;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 552;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    19 GGTGCTTCGGCCCGGCCCGGGAGCGCCGAGCGGGAGAGAGCAGAGAGCAGCCCGAGGG    78
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     8 GGTGCTTCGGCCCGGCCCGGGAGCGCCGAGCGGGAGAGAGCAGAGAGCAGCCCGAGCG    67

Qy    79 CGGGCGGATGCGAGGGGTCCGGGAGGGCGGCACCGGGGAGGAGGAGAGGGGCGCCGCTC   138
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    68 CGGGCGGATGCGAGGGTCGGCGGGCGGCACCGGGCCTCTAAGCTACGACCTCGTCTC    127

Qy   139 CGGCGGCAGCAGGCGGGGGGCCCAGCAGCCTCGGCAGACGACGACGACCGCGGGGCACG   198
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   128 CGGCGGCAGCAGGCGGGGCCCCAGAGCCTCGGCAGCCACAGCCCCTGCGAGCCGGGGCACG   187

Qy   199 CTCCGCTGCTGTCGCGCCTCCTCTGATGCGGCCTTGCGGCCCCGGGACTCCGGGAG    258
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   188 CTCCGCTCGTGTCGCCTCCTCTGATGCGCTCCGGGACTCCGGGAG    247

Qy   259 AATGTGGGGTCCTTAGCGGCCATCCGGGCAACTTTTTTGGGGATTGTTCTTGCTTCCAGGCTTTGC   318
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   248 AATGTGGGGTCCTTAGCGGCCATCCGGGCAACTTTTTTGGGGATTGTTCTTGCTTCCAGGCTTTGC   307

Qy   319 GCTGCAAATCCAGTGTGTCTACCAGTGTGTGAAGAATTCAGCTGAACAACGACTGCTCCTCCC    378
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   308 GCTGCAAATCCAGTGTGTCTACCAGTGTGTGAAGAATTCAGCTGAACAACGACTGCTCCTCCC    367

Qy   379 CGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTCAGAAAAGAAGTGATGGA    438
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   368 CGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTCAGAAAAGAAGTGATGGA    427

Qy   439 GCAAAAGTGCCGGGATCATGTACCGGAACAAGTCCTGTGCCATCATCAGGGCGGGCCCACG    498
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   428 GCAAAAGTGCCGGGATCATGTACCGGAACAAGTCCTGTGCCATCATCAGGGCGGGCCCACG    487

Qy   499 CTCTGCCGGGTACCAGTCCTTCTGTCCTCCCCAGGGAAACTGAACTCAGTTTGCATCACGCG   558
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   488 CTCTGCCGGGTACCAGTCCTTCTGTCCCCAGGGAAACTGAACTCAGTTTGCATCACGCG    547

Qy   559 CTGCAACACCCC    570
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Db   548 CTGCAACACCCC    559
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JOURNAL

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FEATURES             Location/Qualifiers
     source          1..678
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2467075"
                     /clone_lib="NCI_CGAP_Brn25"
                     /tissue_type="anaplastic oligodendroglioma"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGGAGGCGGAGAGGTTTTTTTTTTTTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pT7T3 vector.
                     Library is normalized, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."

BASE COUNT      133 a    199 c    161 g    182 t    3 others
ORIGIN

Query Match     28.8%;  Score 546;  DB 9;  Length 678;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 596;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy  1280 TGCACAGGACTGGCGCCCGGGACGCGCAAGACCAACGGGCGCTGACACAAACGGGCTGTC   1339
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   597 TGCACAGGACTGGCGCCCGGGACGCGCAAGACCAACGGGCGCTGACACAAACGGGCTGTC    538

Qy  1340 GGTGGTGGAGTGGCCCATGTACGCGCCAGGGCGCTTCTTCGTGTGTGCGCACCGACACG   1399
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   537 GGTGGTGGAGTGGCCCATGTACGCGCCAGGGCGCTTCTTCGTGTGTGCGCACCGACACG    478

Qy  1400 GCGGGCAGCACAGCACCTGCACGAACACCCCGCGAAACGTGCTGAGGGACACCCGTGTACAG   1459
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   477 GCGGGCAGCACAGCACCTGCACGAACACCCCGCGAAACGTGCTGAGGGACACCCGTGTACAG    418

Qy  1460 GAGCGCGGTTGATGACCGGACGTGAGGTAGAAAAACGTCTCCGAGAAGGGAGGGAGGATCAT   1519
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   417 GAGCGCGGTTGATGACCGGACGTGAGGTAGAAAAACGTCTCCGAGAAGGGAGGGAGGATCAT    358

Qy  1520 GTACGCCCCGGAAGTAGGACCTTCGTCGTCTGTGCTTGGGGTTTGGGCCGCATGATCCT   1579
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   357 GTACGCGCCGGAAGTAGGACCTTCGTCGTCTGTGCTTGGGGTTTGGGCCGCATGATCCT    298

Qy  1580 CCGGAATCTGGTTGGGGCATCCAGCCATACGGCCAAATGTCACAACAATCAGCCCTGGCAGC   1639
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   297 CCGGAATCTGGTTGGGGCATCCAGCCATACGGCCAAATGTCACAACAATCAGCCCTGGCAGC    238

Qy  1640 ACGAGCAGGAGGGAGACAGAGAGAAAAGAAAAACACAGCATTGAGAACACAGTAAATGAAT   1699
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   237 ACGAGCAGGAGGGAGACAGAGAGAAAAGAAAAACACAGCATGAGAACACAGTAAATAAAT    178

Qy  1700 AAAACCATAAAAATATTTTAGCCCCTCGTTCTCGTGCTTACTGGCCAAGAAATGGTACCAAT   1759
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   177 AAAACCATAAAAATATTTTAGCCCCTCGTTCTCGTGCTTACTGGCCAAGAAATGGTACCAAT    118

Qy  1760 TTTTCAGTGTTGGGACTTGACAGCTTCTTTTGCCACAAGCAAGAGAGAGAGAATTTAACACTGTT   1819
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RESULT 12

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Qy   117 TTTTCAGTGTTGGACTTGACAGCTCTTCTTTTCGCCACAAGCAAGCAAGAGAGAAGTTAACACTGTT 58
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Db  1820 TCAAACCGGGGGAGTTGGCTGTGTTGTTAAAGAAAGACCAATTAAATGCTTTAGACAGTG 1876
Qy  1820 TCAAACCGGGGGAGTTGGCTGTGTTGTTAAAGAAAGACCAATTAAATGCTTTAGACAGTG 1876
Db    57 TCAAACCGGGGGAGTTGGCTGTGTTGTTAAAGAAAGACCAATTAAATGCTTTAGACAGTG 1
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Db	117	BM669397
LOCUS		BM669397 627 bp mRNA linear EST 27-FEB-2002
DEFINITION		UI-E-DW1-ahd-c-11-0-UI.s1 UI-E-DW1 Homo sapiens cDNA clone
		UI-E-DW1-ahd-c-11-0-UI 3', mRNA sequence.
ACCESSION		BM669397
VERSION		BM669397.1 GI:18979294
KEYWORDS		EST.
SOURCE		human.
ORGANISM		Homo sapiens
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE		1 (bases 1 to 627)
AUTHORS		Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE		Normalization and subtraction: two approaches to facilitate gene
		discovery
JOURNAL		Genome Res. 6 (9), 791-806 (1996)
MEDLINE		97044477
COMMENT		Contact: Soares, MB
		Program for Rat Gene Discovery and Mapping
		University of Iowa
		451 Eckstein Medical Research Building Iowa City, IA 52242, USA
		Tel: 319 335 8250
		Fax: 319 335 9565
		Email: msoares@blue.weeg.uiowa.edu
		Tissue Procurement: Dr. Gregg Hageman
		cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
		cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
		DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
		Clone Distribution: Researchers may obtain clones from Research
		Genetics (www.resgen.com).
		Seq primer: M13 Forward
		PolyA=Yes.
FEATURES		Location/Qualifiers
source		1..627
		/organism="Homo sapiens"
		/db_xref="taxon:9606"
		/clone="UI-E-DW1-ahd-c-11-0-UI"
		/clone_lib="UI-E-DW1"
		/tissue_type="lens"
		/dev_stage="adult"
		/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
		/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
		modified polylinker; Site_1: EcoR I; Site_2: Not I;
		UI-E-DW1 is a normalized cDNA library containing the
		following tissue(s): lens. The library was constructed
		according to Bonaldo, Lennon and Soares, Genome Research,
		6:791-806, 1996. First strand cDNA synthesis was primed
		with an oligo-dT primer containing a Not I site. Double
		stranded cDNA was ligated to an EcoR I adaptor, digested
		with Not I, and cloned directionally into pT7T3-Pac
		vector. The oligonucleotide used to prime the synthesis of
		first-strand cDNA contains a library tag sequence that is
		located between the Not I site and the (dT)18 tail. The
		sequence tag for this library is CGATTAGGCA. This library
		was created for the program, Gene Discovery in the Visual
		System, supported by National Eye Institute (NEI).
		TAG_TISSUE=human lens
		TAG_LIB=UI-E-DW1
		TAG_SEQ=CGATTAGGGA"
BASE COUNT		118 a 180 c 145 g 183 t 1 others
ORIGIN		

Query Match   28.7%;   Score 545;   DB 13;   Length 627;
Best Local Similarity   99.8%;
Matches 595; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy  1300 ACGGCGAAGAGCAACGGGGCCGCTGCACAAGCGGGGCTGTCGGTGGGTGGTGCGGCATGTA 1359
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   596 ACGGCGAAGAGCAACGGGGCCGCTGCACAAGCGGGGCTGTCGGTGGGTGGTGCGGCATGTA 537
Qy  1360 CGCGCAGGCGGCCTTCTGCGTGGTGGCCGTCGCAGCGACAGCAGGCGGCGCGACACTGCA 1419
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   536 CGCGCAGGCGGCCTTCTGCGTGGTGGCCGTCGCAGCGACAGCAGGCGGCGCGACACTGCA 477
Qy  1420 CGAACACCCGCCGCGAAACTGCTGCGGAGCAACACCGTGTACAGGAGCGGGGTTGATGACCGGAGC 1479
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   476 CGAACACCCGCCGCGAAACTGCTGCGGAGCAACACCGTGTACAGGAGCGGGGTTGATGACCGGAGC 417
Qy  1480 TGAGGTAGAAAAACGTCTCCGAGAAGGGGAGGGAGGATCATGTACGCCCCGAAGTAGGACC 1539
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   416 TGAGGTAGAAAAACGTCTCCGAGAAGGGGAGGGAGGATCATGTACGCCCCGAAGTAGGACC 357
Qy  1540 TCGTCCAGTGCGTGCTTGGGTTGGGCCGGCCGCCATGAATCTCCGGAATCTCGGTTGGGCATCC 1599
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   356 TCGTCCAGTGCGTGCTTGGGTTGGGCCGGCCGCCATGAATCTCCGGAATCTCGGTTGGGCATCC 297
Qy  1600 AGCATACGGCCAATGTCACAACAATCAGCCCTGGGCAGACAACGCAGGAGAGGGAGAGACA 1659
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   296 AGCATACGGCCAATGTCACAACAATCAGCCCTGGGCAGACAACGCAGGAGAGGGAGAGACA 237
Qy  1660 GAGAAAAACACAACACCATGAGAACACAGTAAATGAATAAAACCATAAAATATTTAGC 1719
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   236 GAGAAAAAGAAAAACACAACACCATGAGAACACAGTAAATAAAATAAAACCATAAAATATTTAGC 177
Qy  1720 CCCTCTGTTCTCGTGCTTACTCGGCCAGGAAATGGTACCAAATTTTTCAGTGTTGGACTTGAC 1779
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   176 CCCTCTGTTCTCGTGCTTACTCGGCCAGGAAATGGTACCAAATTTTTCAGTGTTGGACTTGAC 117
Qy  1780 AGCTTCTTTTGCCACAAGCAAGCAAGAGAGAATTTAACACTGTTTCAAACCCCGGGGGAGTTGGC 1839
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   116 AGCTTCTTTTGCCACAAGCAAGCAAGAGAGAATTAACACTGTTTCAAACCCCGGGGGAGTTGGC 57
Qy  1840 TGTGTTAAAGAAAGACCAATTAAATGCTTTAGACAGTGTAAAAAAAAAAAAAAAAAA 1895
         |||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db    56 TGTGTTAAAGAAAGACCAATTAAATGCTTTAGACAGTGTAAAAAAAAAAAAAAAAA 1
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RESULT 13

Db	117	BF59424/c
LOCUS		BF594242 537 bp mRNA linear EST 12-DEC-2000
DEFINITION		7n10d03.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3564316 3'
		similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
		GPR39. ;, mRNA sequence.
ACCESSION		BF594242
VERSION		BF594242.1 GI:11686566
KEYWORDS		EST.
SOURCE		human.
ORGANISM		Homo sapiens
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE		1 (bases 1 to 537)
AUTHORS		NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE		National Cancer Institute / National Institute of Neurological
		Disorders and Stroke, Brain Tumor Genome Project
		(CGAP/BTGAP), Tumor Gene Index
		Unpublished (1998)
JOURNAL		
COMMENT		Contact: Robert Strausberg, Ph.D.
		Email: cgapbs-r@mail.nih.gov
		Tissue Procurement: David N. Louis, M.D.
		Ph.D.
		cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
		Bonaldo, Ph.D.
		cDNA Library Arrayed by: Greg Lennon, Ph.D.
		DNA Sequencing by: Washington University Genome Sequencing Center
		Clone distribution: NCI-CGAP clone distribution information can be
		found through the I.M.A.G.E. Consortium/LLNL, send email to:
		info@image.llnl.gov

RESULT 14
LOCUS   AI990500   616 bp   mRNA   linear   EST 08-MAR-2000
DEFINITION ws40007.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2499661 3',
            similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
            GPR39.; mRNA sequence.
ACCESSION   AI990500
VERSION   AI990500.1 GI:5837381
KEYWORDS   EST.
SOURCE   human.

FEATURES   Location/Qualifiers
     source   1..616
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2499661"
                     /clone_lib="NCI_CGAP_GC6"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
                     from the normalized library NCI_CGAP_GC4 was prepared, and
                     ss circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (cloneIds
                     1257096-1258631, 1469064-1470983, and 1475592-1476743).
                     Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT   120 a   182 c   147 g   167 t
ORIGIN

Query Match   27.9%; Score 530; DB 9; Length 616;
Best Local Similarity   99.8%; Pred. No. 0; Mismatches 1;
Matches 580; Conservative 0; Indels 0; Gaps 0;

Qy 1297 GGGACGGCGAAGAGCAACGGGCGCGGCGCTGCACAAAGCGGGGGGGCGCCTGTCGTCGGGTGCCGCAT 1356
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 581 GGGACGGCGAAGAGCAACGGGCGCGGCGCTGCACAAAGCGGGGGGGCGCCTGTCGTCGGGTGCCGCAT 522

Qy 1357 GTACGCGCAGGCGCCTTCTCGTGGTTGTGGGGTGCGTGCCAGGGCGGCGAGCAGCAGCGCAGACCT 1416
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 521 GTACGCGCAGGCGCCTTCTCGTGGTTGTGGGGTGCGTGCCAGGGCGGCGAGCAGCAGCGCAGACCT 462

Qy 1417 GCACGAACACCCCGCGAAACTGCTGCGAGGACACCGTGTTACAGGAGGAGGCGCAGACACTTGATGACCG 1476
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 461 GCACGAACACCCCGCGAAACTGCTGCGAGGACACCGTGTTACAGGAGGAGGCGCAGACACTTGATGACCG 402

Qy 1477 AGCTGAGGTAGAAAAAACGTCTCCGAGAAGGAGGAGGAGGAGAAGTCATGTACCCCGGAAGTAGG 1536
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 401 AGCTGAGGTAGAAAAAACGTCTCCGAGAAGGAGGAGGAGGAGAAGTCATGTACCCCGGAAGTAGG 342

Qy 1537 ACCTCGTCCAGTCGTTGCTTGGGTTTGGCCCGCAGCCATGATCCTCCGAATCTGGTTGGGGCA 1596
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 341 ACCTCGTCCAGTCGTTGCTTGGGTTTGGCCCGCAGCCATGATCCTCCGAATCTGGTTGGGGCA 282

Qy 1597 TCCAGCCATACGGCCAATGTCACACAACATCAGCCCTGGCGACACGAGCAGGAGGGGAGAG 1656
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 281 TCCAGCCATACGGCCAATGTCACACAACATCAGCCCTGGCGACACGAGCAGGAGGGGAGAG 222

Qy 1657 ACAGAGAAAAAGAGAAAACACAGCATGAGACACACTAAAAGAACATAAAAAAATATTT 1716
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Db 221 ACAGAGAAAAAGAGAAAACACAGCATGAGACACAGTAAAATAAAAAACCATAAAAATATTT 162

FEATURES   Location/Qualifiers
     source   1..537
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:3564316"
                     /clone_lib="NCI_CGAP_Brn23"
                     /tissue_type="glioblastoma (pooled)"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGGGCCGCCCCATATCTTTTTTTTTTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pT7T3 vector.
                     Library is normalized, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT   107 a   156 c   124 g   150 t
ORIGIN

Query Match   28.3%; Score 537; DB 12; Length 537;
Best Local Similarity   100.0%; Pred. No. 0; Mismatches 0;
Matches 537; Conservative 0; Indels 0; Gaps 0;

Qy 1340 GGTGGTGGAGTGCCCATGTACGCGCCGAGGCCGCCGCCTTCTTCGTGGTTGGCGTGCTGCAGGGACAG 1399
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 537 GGTGGTGGAGTGCCCATGTACGCGCCGAGGCCGCCGCCTTCTTCGTGGTTGGCGTGCTGCAGGGACAG 478

Qy 1400 GCGGCGAGCAGCAGCCACCTGCACGACACACCCCGGGAAAACGTCGTCGAGGAACCGTGTACAG 1459
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 477 GCGGCGAGCAGCAGCCACCTGCACGACACACCCCGGGAAAACGTCGTCGAGGAACCGTGTACAG 418

Qy 1460 GAGCGCGGGTTGATGACCGAGCTGAGGTAGAAAAAACGTCTCCGAGAAGGAGGAGGAGGATCAT 1519
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 417 GAGCGCGGGTTGATGACCGAGCTGAGGTAGAAAAAACGTCTCCGAGAAGGAGGAGGAGGATCAT 358

Qy 1520 GTACGCCCGGAAGTAGGAACCTCGTCCAGTCGTCGCTGCTTGGGGTTGGCCCGCAGCCATGATCCT 1579
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 357 GTACGCCCGGAAGTAGGAACCTCGTCGTCGCTGCTTGGGGTTGGCCCGCAGCCATGATCCT 298

Qy 1580 CCGAATCTGGTTGGGGCCATCCAGCCAATGTCACACAACAATCAGCCCTGGGCGACAC 1639
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 297 CCGAATCTGGTTGGGGCCATCCAGCCAATGTCACACAACAATCAGCCCTGGGCGACAC 238

Qy 1640 ACGAGCAGGAGGGGAGGAGAAAAAGAGAAAACACAGCATGAGAACACACTAAAATGAAT 1699
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 237 ACGAGCAGGAGGGGAGGAGAAAAAGAGAAAACACAGCATGAGAACACACTAAAATGAAT 178

Qy 1700 AAAACCATAAAAATATTTAGGCCCCTCTCGTCTTCTCGTGTTCTGGCCACGGAAAATGGTACCAAT 1759
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 177 AAAACCATAAAAATATTTAGCCCTCTCGTCTTCTCGTGTTCTGGCCACGGAAATGGTACCAAT 118

Qy 1760 TTTTCAGTGTTGGACTTGACAGCTTCTTTTTTGCCACAAGCAAGAGAAATTTAACACTGTT 1819
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 117 TTTTCAGTGTTGGACTTGACAGCTTCTTTTGCCACAAGCAAGAGAAATTTAACACTGTT 58

Qy 1820 TCAAACCCGGGGGGGAGTTGGCTGTCGTGTTAAAGAAAGACCATTAAAATGCTTTAGACAGTG 1876
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   57 TCAAACCCGGGGGGGAGTTGGCTGTCGTGTTAAAGAAAGACCATTAAAATGCTTTAGACAGTG 1

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Qy  1717 AGCCCCTCTGTTCTGTGCTTACTGCCCCAGGAAAATGGTACCAATTTTTTCAGTGTTGGACTT 1776
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   161 AGCCCCTCTGTTCTGTGCTTACTGGCCCAGGAAAATGGTACCAATTTTTTCAGTGTTGGACTT 102

Qy  1777 GACAGCTTCTTTTGCCACAAGCAAGAGAGAGAGAGAATTTAAACACTGTTTCAAACCCGGGGGGGAGTT 1836
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   101 GACAGCTTCTTTTGCCACAAGCAAGAGAGAGAGAGAATTTAAACACTGTTTCAAACCCGGGGGGGAGTT 42

Qy  1837 GGCTGTGTTAAAGAAAGACCATTAAATGCTTTAGACAGTGT 1877
         |||||||||||||||||||||||||||||||||||||||||
Db    41 GGCTGTGTTAAAGAAAGACCATTAAATGCTTTAGACAGTGT 1
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RESULT 15
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LOCUS       AW590950/c               649 bp    mRNA    linear    EST 22-MAR-2000
DEFINITION  AW590950 hg51e12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2949166 3'
            similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
            GPR39. ;, mRNA sequence.
ACCESSION   AW590950
VERSION     AW590950.1  GI:7278094
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 649)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            Image.llnl.gov/image/html/iresources.shtml
            Possible reversed clone: similarity on wrong strand
            Seq primer: -40UP from Gibco
            High quality sequence stop: 457.
FEATURES             Location/Qualifiers
     source          1..649
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:2949166"
                     /clone_lib="NCI_CGAP_GC6"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: p7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
                     from the normalized library NCI_CGAP_GC4 was prepared, and
                     ss circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (cloneIds
                     1257096-1258631, 1469064-1470983, and 1475592-1476743).
                     Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT    132 a    189 c    155 g    173 t
ORIGIN
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Query Match   27.3%;  Score 517;  DB 10;  Length 649;
Best Local Similarity  99.8%;
Matches  567;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy  1310 CAACGGGGCGCTGCACAAAGCGGGGCGCGTGTCGGTGGTGAGTGCCAGTACCCGCAGGCG 1369
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db   568 CAACGGGGCGCTGCACAAAGCGGGGCGCGTGTCGGTGGTGAGTGCCAGTACCCGCAGGCG 509
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1370 CTTCTCGTGGTTGGCGTGCTGCAGGCAGCAGAGGCGGCAGCGACACAGCGACCTTGCGCA 1429
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Db   508 CTTCTCGTGGTTGGCGTGCTGCAGGCAGCAGAGGCGGCAGCGACACAGCGACCTTGCGCA 449

Qy  1430 CCGAAAACTGCGTGCGAGGACACCGGTGCTGCACAGGAGCGGGTTGAGTGGAGTGCGGA 1489
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   448 CCGAAAACTGCGTGCGAGGACACCGGTGCTGCACAGGAGCGGGTTGAGTGGAGTGCGGA 389

Qy  1490 AAACGTCTCCGAGAAGGGGAGGAGGAGGGATCATGTACGCCCGGAGTAGGACCTCGTCCAGTC 1549
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   388 AAACGTCTCCGAGAAGGGGAGGAGGAGGGATCATGTACGCCCGGAGTAGGACCTCGTCCAGTC 329

Qy  1550 GTGCTTGGGTTTGGCCCGCAGGAAATCGTACCAATTTTTCAGTGTTGGGCCATCCAGCATACGGC 1609
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   328 GTGCTTGGGTTTGGCCCGCAGGAAATCGTACCAATTTTTCAGTGTTGGGCCATCCAGCATACGGC 269

Qy  1610 CAATGTCACACAATCAGCCCTGGGCAGACACGGGGGGAGAGGAGGAAAAGA 1669
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   268 CAATGTCACACAATCAGCCCTGGGCAGACACGGGGGGAGAGGAGGAAAAGA 209

Qy  1670 AAACACAGCATGAGAACACAGTAAAATGAATAAAACCATTAAAATATTTAGCCCCTTCGTTC 1729
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   208 AAACACAGCATGAGAACACAGTAAAATAAAATATTTTCAGTGTTGGACTTGACACGTTCTTTTT 149

Qy  1730 TGTGCTTACTGGCCAGGAAATGGTACCAATTTTTCAGTGTTGGACTTGACACGTTCTTTTT 1789
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   148 TGTGCTTACTGGCCAGGAAATGGTACCAATTTTTCAGTGTTGGACTTGACACGTTCTTTT 89

Qy  1790 GCCACAAGCAAGAGAGAGAGAAATTTAACACTGTTTCAAACCCGGGGGGGAGTTGGCTGTGTTAAAG 1849
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    88 GCCACAAGCAAGAGAGAGAGAAATTTAACACTGTTTCAAACCCGGGGGGGAGTTGGCTGTGTTAAAG 29

Qy  1850 AAAGACCATTAAATGCTTTAGACAGTGT 1877
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Db    28 AAAGACCATTAAATGCTTTAGACAGTGT 1
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RESULT 16
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LOCUS       BE858216/c               551 bp    mRNA    linear    EST 29-SEP-2000
DEFINITION  BE858216 7g19g07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3306972 3'
            similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
            GPR39. ;, mRNA sequence.
ACCESSION   BE858216
VERSION     BE858216.1  GI:10372861
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 551)
AUTHORS     NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTGAP), Tumor Gene Index
JOURNAL     Unpublished (1998)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
            Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco
            High quality sequence stop: 490.
FEATURES             Location/Qualifiers
     source          1..551
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                    /organism="Homo sapiens"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:3306972"
                    /clone_lib="NCI_CGAP_Brn23"
                    /tissue_type="glioblastoma (pooled)"
                    /lab_host="DH10B"
                    /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
                    modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                    strand cDNA was primed with a Not I - oligo(dT) primer [5'
                    TGTTACCAATCTGAAGTGGGAGCGGCGGCCGCCAATAGTTTTTTTTTTTTTTTTTTTT
                    T-3'], double-stranded cDNA was ligated to Eco RI
                    adaptors (Pharmacia), digested with Not I and cloned into
                    the Not I and Eco RI sites of the modified pT7T3 vector.
                    Library is normalized, and was constructed by Bento
                    Soares and M.Fatima Bonaldo."
BASE COUNT      110 a      161 c      128 g      152 t
ORIGIN

Query Match      26.4%;  Score 500;  DB 12;  Length 551;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 550;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy  1327  AGCGGGCGCTGCGGTGGTGGCGGCCATGTACGGCGGAGGCCCATGTTCTCGTCGGTTGGCGT 1386
          ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db   551  AGCGGGCGCTGCGGTGGTGGAGTGCGGCATGTACGGCGGAGGCCCATGTTCTCGTCGGTTGGCGT 492

Qy  1387  GCTGCAGCGACAGGCGGCGCAGCAGCAGCACACCTGCACGAACAGAACTGCTGCGAGG 1446
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   491  GCTGCAGCGACAGGCGGCGCAGCAGCAGCACACCTGCACGAACAGAACTGCTGCGAGG 432

Qy  1447  ACACCGTGTACAGGAGGAGGCGGTTGATGACCGAGGTAGAAAAACGTCTCCGAGAAGG 1506
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   431  ACACCGTGTACAGGAGGAGGCGGTTGATGACCGAGGTAGAAAAACGTCTCCGAGAAGG 372

Qy  1507  GGAGGAGGATCAATGTACGGCCCGGAAGCTAGGAGCCTCCTCCAGTCGCCTTGGGTTTGGCCG 1566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   371  GGAGGAGGATCAATGTACGGCCCGGAAGCTAGGAGCCTCCTCCAGTCGCCTTGGGTTTGGCCG 312

Qy  1567  CAGCCATGATCCTCCGGAATCTGGTTGGGCCATGCAATAGTCACAACAATCA 1626
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   311  CAGCCATGATCCTCCGGAATCTGGTTGGGCCATGCAATAGTCACAACAATCA 252

Qy  1627  GCCCTGGGCAGACACGAGAGGAGAGAGAGAAAAACAGAACATGAGAAC 1686
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Db   251  GCCCTGGGCAGACACGAGAGGAGAGAGAGAAAAACAGAACATGAGAAC 192

Qy  1687  ACAGTAAATGAATAAAAACCATAAAAATATTTAGCCCCTCTGTTTCTTCTTACTGGCCAGG 1746
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   191  ACAGTAAATAAATAAAAACCATAAAAATATTTAGCCCCTCTGTTTCTTCTTACTGGCCAGG 132

Qy  1747  AAAATGGTACCAATTTTTCAGTGTGTTGGACTTGACAGCTTCTTTTTGCCACAAGCAAGAGAGA 1806
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Db   131  AAAATGGTACCAATTTTTCAGTGTGTTGGACTTGACAGCTTCTTTTTGCCACAAGCAAGAGAGA 72

Qy  1807  ATTTAACACTGTTTCAAACCCGGGGAGTTGGCTGTCGTTAAAGAAAAGACCCATTAAATGCT 1866
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    71  ATTTAACACTGTTTCAAACCCGGGGAGTTGGCTGTGTTAAAGAAAAGACCATTAAATGCT 12

Qy  1867  TTAGACAGTGT 1877
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Db    11  TTAGACAGTGT 1
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REFERENCE   1  (bases 1 to 698)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/,
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11784  row: d  column: 08
            High quality sequence stop: 687.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

FEATURES             Location/Qualifiers
     source          1..698
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="NCI_CGAP_Brn67"
                     /tissue_type="anaplastic oligodendroglioma with 1p/19q
                     loss"
                     /clone="IMAGE:5309527"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 2.3 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      131 a      231 c      204 g      132 t
ORIGIN

Query Match      26.3%;  Score 498;  DB 13;  Length 698;
Best Local Similarity   99.8%;  Pred. No. 0;
Matches 618;  Conservative  0;  Mismatches  0;  Indels  1;  Gaps  1;

Qy    19  GGTGCCTCGGCGCCCCGGGAGGCGGAGGAGGACAGAGAGACCCGGCAGCCGGGAGCCGAGCG 78
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    17  GGTGCCTCGGCGCCCCGGGAGGCGGAGGAGGACAGAGAGACCCGGCAGCCGGGAGCCGAGCG 76

Qy    79  CGGGCGGATGCGACAGGCCGCTCCGCCGGAGGGCGCCACCTGCGCCGGCTCCTCTCAAGCTTACGAACCGTCGTCGTCTC 138
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    77  CGGGCGGATGCGACAGGCCGCTCCGCCGGAGGGCGCCACCTGCGCCGGCTCCTCTCAAGCTTACGAACCGTCGTCGTCTC 136

Qy   139  CGGGGCGAGAGCGGGGCGGGCCCCAGAGCCGCTCGCAGCCCACGAGCCGCTGCGACGCGGGGCAGC 198
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   137  CGGGGCAGCAGGCGGGCCGCCCCAGAGCCGCTCGCAGCCCACGAGCCGCTGCGACGCGGGGCAGC 196

Qy   199  CTCCGCTGCGTCGCCTCCTCGATGGCGCTGCCCCTTCTCCCGGCGGCGCCCGGGGACTCGGGGAG 258
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   197  CTCCGCTGCGTCGCCTCCTCGATGGCGCTGCCCCTTCTCCCGGCGGCGCCCGGGGACTCGGGGAG 256

Qy   259  AAATGTGGGTCGTCCTAGGCCATGCGGCCAACTTTTTTGGGATTGTGTTCTTGCTTCCAGCGTTTGC 318
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   257  AAATGTGGGTCCTAGGCCATGCGGCCAACTTTTTTGGGATTGTGTTCTTGCTTCCAGCGTTTGC 316

Qy   319  GCTGCAAATCCAGTGCTACCAGTGTGAAGAATTCCAGCGTGAACAAACGACTGCTCCTCCCC 378
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   317  GCTGCAAATCCAGTGCTACCAGTGTGAAGAATTCCAGCGTGAACAAACGACTGCTCCTCCCC 376

Qy   379  CGAGTTCATTGTGAATTGCACGGTGCACGGTTCAAGACACATGTCAGAAG-GAAGTGATGG 438
          |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   377  CGAGTTCATTGTGAATTGCACGGTGCACGGTTCAAGACACATGTGTCAGAAAACGAAGTGATGG 437

Qy   438  AGCAAAGTGCCGGGATCAGTGTACCGCAAGTCCTTGCATCATCACCGGCCGCTGTTCATCG 497
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   437  AGCAAAGTGCCGGGATCAGTCATGTACCGCAAGTCCTTGCATCATCACCGGCCGCTGTTCATCG 496

Qy   498  CCTCTGCCGGGTACCAGTCCTTTCTGCTCCCCAGGGAAACTGAACTCAGTTTGCATCAGCT 557
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   497  CCTCTGCCGGGTACCAGTCCTTTCTGCTCCCCAGGGAAACTGAACTCAGTTTGCATCAGCT 556
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RESULT 17
LOCUS       BI554034     698 bp    mRNA    linear    EST   05-SEP-2001
DEFINITION  603254826F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:5309527
            5', mRNA sequence.
ACCESSION   BI554034
VERSION     BI554034.1  GI:15441348
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
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RESULT 18

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Qy    558  GCTGCAACACCCCTTCTTTGTAACGGGCCAAGGCCCAAGAAAAAGGGGAAGTTCTGCCTCGG  617
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    557  GCTGCAACACCCCTTCTTTGTAACGGGCCAAGGCCCAAGAAAAAGGGGAAGTTCTGCCTCGG  616

Qy    618  CCCTCAGGCCAGGGCTCCG  636
           |||||||||||||||||||
Db    617  CCCTCAGGCCAGGGCTCCG  635
```

```
LOCUS       BF939693/c
DEFINITION  BF939693  nac80b12.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3440591 3'
            similar to SW:GP39_HUMAN 043194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
            GP39. ;, mRNA sequence.
ACCESSION   BF939693
VERSION     BF939693.1  GI:12357104
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 540)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTGAP), Tumor Gene Index
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
            Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco
            High quality sequence stop: 467.
FEATURES             Location/Qualifiers
     source          1..540
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3440591"
                     /clone_lib="NCI_CGAP_Brn23"
                     /tissue_type="glioblastoma (pooled)"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGACGGCCGCCCATAATCTTTTTTTTTTTTTTTTTTTTTTTTT
                     T 3'], double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pT7T3 vector.
                     Library is normalized, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT       108 a    158 c    124 g    150 t
ORIGIN
```

Query Match   25.8%; Score 489; DB 12; Length 540;
Best Local Similarity   99.8%;
Matches 539; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Qy   1337  GTCGGTGTGGTGGAGTGCCCATGTACGCCCCAGGGCGCCTTCGTTGGTTGTCGTGCCAACGA  1396
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540  GTCGGTGTGGTGGAGTGCCCATGTACGCCCCAGGGCGCCTTCGTTGGTTGTCGTGCCAACGA  481

Qy   1397  CAGGCGCGCAGCAGCACCTGCACGAACACCCGGCAGAAACTGCTGCCAGGACACCGTGTA  1456
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480  CAGGCGCGCAGCAGCACCTGCACGAACACCCGGCAAAACTGCTGGAGGACACCGTGTA  421
```

RESULT 19

```
LOCUS       AI742092/c
DEFINITION  AI742092  wg38h03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
            IMAGE:2367413 3' similar to SW:GP39_HUMAN 043194 PUTATIVE G
            PROTEIN-COUPLED RECEPTOR GP39. ;, mRNA sequence.
ACCESSION   AI742092
VERSION     AI742092.1  GI:5110380
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 578)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 806   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 460.
FEATURES             Location/Qualifiers
     source          1..578
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2367413"
                     /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
                     /lab_host="DH10B"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Equal amounts of plasmid DNA from five normalized
                     libraries were mixed, and ss circles were made in vitro.
                     Following HAP purification, this DNA was used as tracer in
                     a subtractive hybridization reaction. The driver was
                     PCR-amplified cDNAs from pools of 5,000 clones made from
                     the same 5 libraries. The pools consisted of the following
                     libraries and cloneIDs: Soares NbHSF pool 1:
                     309384-310919, 323208-325895 Soares Nb2HP pool 1:
                     145032-147335, 147720-148103, 148872-149255, 15002 -
                     150407, 151176-152327 Soares Nb2HF8-9W pool 1:
```

```
Qy   1457  CAGGAGGGGGTTGATGACCGAGCTGAGGTAGAGGTAGAAACGTCTCCGAGAAGGGGAGGAGGAT  1516
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420  CAGGAGGCGGGTTGATGACCGAGCTGAGGTAGAGGTAGAAACGTCTCCGAGAAGGGGAGGAGGAT  361

Qy   1517  CATGTACGCCCCGGAAGTAGGAACCTCGTCCAGTCGTCGTTGGGTTTGGCCGCCAACCATGAT  1576
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    360  CATGTACGCCCCGGAAGTAGGAACCTCGTCCAGTCGTCGTTGGGTTTGGCCGCCAACCATGAT  301

Qy   1577  CCTCCGAAATCTGGTTGGGCATCCAGCATCATACGGCCCAATGTCACAACAATCAGCCCTGGGCA  1636
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300  CCTCCGAAATCTGGTTGGGCATCCAGCATACGGCCCAATGTCACAACAATCAGCCCTGGGCA  241

Qy   1637  GACACGAGCAGGAGGAGGAGGAGGAGGAAAAACACAGCAATGAGAACAGCAGTAAATG  1696
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    240  GACACGAGCAGGAGGAGGAGGAGGAGGAAAAACACAGCAATGAGAACAGCAGTAAATG  181

Qy   1697  AATAAAAACCATAAAAATATTTAGCCCCCTCGTCTTGCTTACTGGCCAGGAAATGGTACC  1756
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    180  AATAAAAACCATAAAAATATTTAGCCCCCTCGTCTTGCTTACTGGCCAGGAAATGGTACC  121

Qy   1757  AATTTTTTCAGTGTTGGACTTGACAGCTTCTTTTTGCCACAAGCAAGAGAGAATTTAACACT  1816
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    120  AATTTTTTCAGTGTTGGACTTGACAGCTTCTTTTTGCCACAAGCAAGAGAGAATTTAACACT  61

Qy   1817  GTTTTCAAAACCCCGGGGGAGTTGGCTGTTAAGAAAGACCATTAAATGCTTTAGACAGTG  1876
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     60  GTTTTCAAAACCCCGGGGGAGTTGGCTGTTGTTAAGAAAGACCATTAAATGCTTTAGACAGTG  1
```

758280-760583, 772104-774407 Soares NbHPa pool 1:
304776-306311, 320136-322823, 326280-326663 Soares NbHOT
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT   102 a   176 c   142 g   158 t
ORIGIN

Query Match   25.5%;   Score 484;   DB 9;   Length 578;
Best Local Similarity   99.8%;
Matches 534; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

```
Qy   1152  TCTGCAGCAGAATTGGCTGGTTTCCGCCTCAGTTGGGCTCTAGTGACTCCAGACTCAAT  1211
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    574  TCTGCAGCAGAATTGGCTGGTTTCCGCCTCAGTTGGGCTCTAGTGACTCCAGACTCAAT   515

Qy   1212  GACTGGGACTTAGACTGGGCGTCGGGGCTCGCGGCTCCTCGTCGAAAAGTGCTTAAGAAAAATCTTCTCA  1271
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1213  GACTGGGACTTAGACTGGGCGTCGGGGCTCGCGGCTCCTCGTCGAAAAGTGCTTAAGAAAAATCTTCTCA   455

Qy   1272  GTTCTTCCTTCCAGAGGAGGACTGGCCCCGGACCCGGAAGAGCAACAGCGGCTGCACAAAGCGG  1331
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    454  GTTCTTCCTTCCAGAGGAGGACTGGCCCCGGGACGCGGAAGAGCAACAGCGGCTGCACAAAGCGG   395

Qy   1332  GCGCTGTCGGTGGTGGGAGTGCGGCCATGTACCGGCGCGCTTCTTCGTTCGTTGGCGTGCTGC  1391
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394  GCGCTGTCGGTGGTGGGAGTGCGGCCATGTACCGGCGCGCTTCTTCGTTCGTTGGCGTGCTGC   335

Qy   1392  AGCGACAGAGGGCGGCCAGCACACCACCTGCACAAAACTGTCTGCGGAGGACACC  1451
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    334  AGCGACAGAGGGCGGCCAGCACACCACCTGCACAAAACTGTCTGCGGAGGACACC   275

Qy   1452  GTGTACAGGAGGACGCGGGGTTGATGACCGAGCTGAGGTAGTACAACACCCCGGAAGGGGAGG  1511
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274  GTGTACAGGAGGACGGGGTTGATGACCGAGCTGAGGTAGTACAACACCCCGGAAGGGGAGG   215

Qy   1512  AGGATCATGTACGGCCCCGGAAGTAGGACCTCGTCCAGTCGTGTCGTTGGGTTTGGCGCCAGCC  1571
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    214  AGGATCAATGTACGGCCCCGGAAGTAGGACCTCGTCCAGTCGTGTCGTTGGGTTTGGCGCCAGCC   155

Qy   1572  ATGATCCTCCGAAATCTTGGTTCGGGCATCCAGCATTACGGCCAATGTCACAACAATCAGCCCT  1631
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    154  ATGATCCTCCGAAATCTTGGTTCGGGCATCCAGCATTACGGCCAATGTCACAACAATCAGCCCT    95

Qy   1632  GGGCAGCACCAGCGGGAGGAGGAGGAGGACGAGGAGAAAAAGAAAAAACACAGCGATGAGAAC  1686
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     94  GGGCAGCACCAGCAGGAGGAGGAGGAGGACGAGGAGAAAAAGAAAAAACACAGCATGAGAAC    40
```

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 408.

FEATURES   Location/Qualifiers
     source   1..534
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3146086"
                     /clone_lib="NCI_CGAP_Kid13"
                     /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                     Library constructed by Life Technologies."
                     /tissue_type="2 pooled Wilms' tumors, one primary and one
                     metastatic to brain"
                     /lab_host="DH10B"

BASE COUNT   98 a   172 c   143 g   121 t
ORIGIN

Query Match   25.3%;   Score 479;   DB 10;   Length 534;
Best Local Similarity   99.8%;
Matches 529; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

```
Qy   1131  TCATGCTCCTGAAAACCATTCTCTGCACGAGAAGAATTGGCTGGTTCGGCGTTGGGTTTCGCGGCCTGAGTTGGGC  1190
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    530  TCATGCTCCTGAAAACCATTCTCTGCACGAGAAGAATTGGCTGGTTCGGCGTTGGGTTTCGCGGCCTGAGTTGGGC   471

Qy   1191  TCTAGTGACTCGAGACTCAATGACTGGGACTTAGACTGGGCGTCGGGGCTCGGCCCTCGCTGTGAAAA  1250
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    470  TCTAGTGACTCGAGACTCAATGACTGGGACTTAGACTGGGCGTCGGGGCTCGGCCCTCGCTGTGAAAA   411

Qy   1251  GTGCTTAAGAAAAATCTTCTCAGTTCTTCCTTGCAGAGGAGGACTGGGCGCCGGGACGGGAAGAGCC  1310
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    410  GTGCTTAAGAAAAATCTTCTCAGTTCTTCCTTGCAGAGGAGGACTGGGCGCCGGGACGGGAAGAGC   351

Qy   1311  AACGGGCGCGGTTGCACAAAGCGGGGGCGCGGTGTGGAGTGCGATGTACGGCGCAGGCGC  1370
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    350  AACGGGCGCGGTTGCACAAAGCGGGGGCGCGGTGTGGAGTGCGATGTACGGCGCAGGCGC   291

Qy   1371  TTCTCGTGGTGTTGGGGTGCTGCAGCGACAGAGGCGCAGCAGCAACGACACCCGC  1430
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    290  TTCTCGTGGTGTTGGGGTGCTGCAGCGACAGAGGCGCAGCAGCAACGACACCCGC   231

Qy   1431  CGAAACTCGTCGCGAGGACACCGTGTACAGGAGGACGGGGTTGATGACCGACTGAGGTAGAAA  1490
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    230  CGAAACTCGTCGCGAGGACACCGTGTACAGGAGGACGGGGTTGATGACCGACTGAGGTAGAAA   171

Qy   1491  AACGTCTCCGAGAAGGGAGGAGGAGGATCATTGTACGGCCCCGGAAGAGTAGGACCTCGTCCAGTCG  1550
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    170  AACGTCTCCGAGAAGGGAGGAGGAGGATCATTGTACGGCCCCGGAAGAGTAGGACCTCGTCCAGTCG   111

Qy   1551  TGCTTGGGTTTGGCGCGACCAGCCATGATCATGATCCTCCGAAATCCTTGGTTCGGGCATTACGGGC  1610
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    110  TGCTTGGGTTTGGCGCGACCAGCCATGATCATGATCCTCCGAAATCCTTGGTTCGGGCATTACGGGC    51

Qy   1611  AATGTCACAACAATCAGCCCTGGGCCGCAGCAGGAGGAGGAGGACACAG  1660
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     50  AATGTCACAACAATCAGCCCTGGGCCGCAGCAGGAGGAGGAGGACACAG     1
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RESULT 21
AW338938/c
LOCUS   AW338938   527 bp   mRNA   linear   EST 31-JAN-2000
DEFINITION ha68h04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2878903 3'
            similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
            GPR39.;, mRNA sequence.
ACCESSION   AW338938
VERSION   AW338938.1 GI:6835564
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

RESULT 20
BE350014/c
LOCUS   BE350014   534 bp   mRNA   linear   EST 18-JUL-2000
DEFINITION ht07g12.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146086 3'
            similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
            GPR39.;, mRNA sequence.
ACCESSION   BE350014
VERSION   BE350014.1 GI:9261867
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 534)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Chris Moskaluk, M.D., Ph.D.
            Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
            Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
            I.M.A.G.E. Consortium DNA Sequencing by: Washington University
            Genome Sequencing Center

REFERENCE   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS   1 (bases 1 to 527)
TITLE   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
             National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
             Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Life Technologies catalog #: 11548-013
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             www-bio.llnl.gov/bbrp/image/image.html

             Possible reversed clone: similarity on wrong strand
             Seq primer: ~40UP from Gibco
             High quality sequence stop: 420.

FEATURES   Location/Qualifiers
source   1..527
             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /clone="IMAGE:2878903"
             /clone_lib="NCI_CGAP_Pan1"
             /tissue_type="adenocarcinoma"
             /note="Organ: Pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
             Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT;
             Average insert size 1.72 kb. Life Technologies catalog #:
             11548-013"
             /lab_host="DH10B"

BASE COUNT   103 a   143 c   120 g   161 t
ORIGIN

Query Match
Best Local Similarity   99.8%;   Score 476;   DB 10;   Length 527;
Matches 526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;   Pred. No. 0;

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Qy 1364 CAGGCGCTTCTCGTTCGGTGGTTGGCGTTGGCGTTGGCGTCGGACGAGACGACCTGCACGAA 1423
        |||||||||||||||||||||||||||||||      |||||  |  |||    || ||||
Db  527 CAGGCGCTTCTCGTTCGGTGGTTGGCGTCGTCGCAGGCGACCAGGCGGCGGCGCCAGCGAA 468

Qy 1424 CACCCGCGCGAAACTGCTCGCCGAGAGACACCGTGTACAGGAGGGGGTTGATGACCGACTGAG 1483
        |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  467 CACCCGCCCAAACTGCTCGCCGAGAGACACCGTGTACAGGAGGGGGTTGATGACCGACTGAG 408

Qy 1484 GTAGAAAAAACGTCTCCGAGAAGGGGGAGAGGAGGATCATGTTACGCCCCGGAAGTAGGACCTCGT 1543
        |||||||| ||||||||||||||||||||||||||||||| ||||||| |||||||||||||||
Db  407 GTAGAAAAACGTCTCCGAGAAGGGGGAGAGGAGGATCATGTGACGCCCGGAAGTAGGACCTCGT 348

Qy 1544 CCAGTCGTGTCCTTGGGTTTGGCCCGGCCACCATGATCCTCCGAAATCGTTGGGCATCCAGCA 1603
        |||||||| ||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db  347 CCAGTCGTGCCTTGGGTTTGGCCCGGCCATGATCCTCCGAAATCGTTGGGCATCCAGCA 288

Qy 1604 TACGGGCCAAATGTCACACAACAATCAGCCCTGGGCAGACACGAGCAGGAGGAGAGACAGAGA 1663
        |||||| ||| ||||||||||  |||||||||||||||||||| ||||||||||||||||||
Db  287 TACGGCCAATGTCACACAAATCAGCCCTGGGCAGACACGAGGAGGAGGAGAGACAGAGA 228

Qy 1664 AAAGAAAAACACAGCATGAGAACACATAGAAAGTAAAATGAAATAAAACACTTAAAAATATTTAGCCCCT 1723
        |||||||||||||||||||||||||  |    ||  |||  |   |||| |||||||||||||||||||
Db  227 AAAGAAAAACACAGCATGAGAACACAGTAAAATAAATAAAACCATTAAAAATATTTAGCCCCT 168

Qy 1724 CTGCTTCTGTGCTTACTGCCCAGGAAATGGTACCAANTTTTTCAGTGTTGGGACTTGACAGCT 1783
        ||| ||||||||||||||||||||||||||| ||||  |||||||||||||||||||||||||
Db  167 CTGTTCTGTGCTTACTGCCCAGGAAATGGTGCCAATTTTTCAGTGTTGGGACTTGACAGCT 108

Qy 1784 TCTTTTGCCACACAAGCAGAAGAGAAGGAAGAATTTAACACTGTTCAAACCCGGGGGAGTTGGGCTGTG 1843
        |||||||||||||||||||   | |  |  ||||||||||||||||||||||||||||||||||||||
Db  107 TCTTTTGCCACACAAGCAGAGAGAATTTAACACTGTTCAAACCCGGGGGAGTTGGGCTGTG 48

Qy 1844 TTAAAGAAAGACCCATTAAAATGCTTTAGACAGTGTAAAAAAAAAAAAAA 1890
        |||||||||||||||||||||||||||||||||||||||||||||||
Db   47 TTAAAGAAAGACCCATTAAAATGCTTTAGACAGTGTAAAAAAAAAAAAAA 1
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RESULT 22
BI913989
LOCUS   BI913989   707 bp   mRNA   linear   EST 16-OCT-2001
DEFINITION 603180565F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5244569 5',
            mRNA sequence.
ACCESSION   BI913989
VERSION   BI913989.1 GI:16178286
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 707)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM1617 row: a column: 18
            High quality sequence stop: 698.

FEATURES   Location/Qualifiers
source   1..707
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:5244569"
            /clone_lib="NIH_MGC_121"
            /lab_host="DH10B"
            /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
            Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
            fetal brains, female age 20 weeks, female age 24 weeks,
            and male age 26 weeks. Library is oligo-dT primed and
            directionally cloned (EcoRV site is destroyed upon
            cloning). Average insert size 1.7 kb, insert size range
            0.7-3.5 kb. Library is normalized and enriched for
            full-length clones and was constructed by C. Gruber
            (Invitrogen). Research Genetics tracking code 017. Note:
            this is a NIH_MGC Library."

BASE COUNT 133 a   209 c   209 g   132 t
ORIGIN

Query Match
Best Local Similarity   100.0%;   Score 476;   DB 13;   Length 707;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;   Pred. No. 0;

```
Qy 153 GGGGCCCCAGCAGCCCTGGGCAGCCCACAGCCCGTGTCAGCCGCGGGGGGGCAGCCTCCGCTGCTGTCG 212
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 159 GGGCCCCAGCAGCCCTGGGCAGCCCACAGCCCGTGTCAGCCGCGGGGGGGCAGCCTCCGCTGCTGTCG 218

Qy 213 CCTCCTCTGATGCGCTTGCCCTCTCCCGGCCCCGGGGGACTCCGGGGAGGAATGGGGTCCTAG 272
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 219 CCTCCTCTGATGGCGCTTGCCCTCTCCCGGCCCCGGGGGGAGACTCCGGGAGAATGGGGTCCTAG 278

Qy 273 GCATCGGCGCAACTTTTTGCGGATTGGTTCTTGCCTTCCAGGCTTTGCGCTGCAAATCCAGT 332
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 279 GCATCGGCGCAACTTTTTGCGGATTGGTTCTTGCCTTCCAGGCTTTGCGCTGCAAATCCAGT 338

Qy 333 GCTACCAGTGTGAAGAAATTCCAGCTGAACAACGACTGCTTCTCTCCCCCGAGTTCATTGTGA 392
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 339 GCTACCAGTGTGAAGAAATTCCAGCTGAACAACGACTGCTTCTCTCCCCCGAGTTCATTGTGA 398

Qy 393 ATTGCACGGTGAACGTTCAGACACATGTGTCAGAAAGAAGTGATGGAGCAAAGTGCCGGGA 452
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 399 ATTGCACGGTGAACGTTCAGACACATGTGTCAGAAAGAAGTGATGGAGCAAAGTGCCGGGA 458

Qy 453 TCATGTACCGCCAAGTCCGTGCATCATCAGGCGCCGTGTCTCATCAGGCGCCTCGCGGGGTACC 512
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

RESULT 23

```
LOCUS       BF726459                   530 bp    mRNA    linear   EST 05-JAN-2001
DEFINITION  by06h03.y1 Human Lens cDNA (Un-normalized, unamplified): BY Homo
            sapiens cDNA clone by06h03 5', mRNA sequence.
ACCESSION   BF726459
VERSION     BF726459.1  GI:12042370
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 530)
AUTHORS     Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.
TITLE       NEIBANK: EST analysis and bioinformatics for ocular genomics
JOURNAL     Invest. Ophthalmol. Vis. Sci. 41, (2000) In press
COMMENT     Contact: Wistow G
            Section on Molecular Structure and Function
            National Eye Institute
            6/331, NIH, Bethesda, MD 20892-2740, USA
            Tel: 301 402 3452
            Fax: 301 496 0078
            Email: graeme@helix.nih.gov
            Plate: 06  row: h  column: 03
            Seq primer: M13R1 reverse primer (ABI).
FEATURES             Location/Qualifiers
    source          1..530
                    /organism="Homo sapiens"
                    /db_xref="taxon:9606"
                    /clone="by06h03"
                    /clone_lib="Human Lens cDNA (Un-normalized, unamplified):
                    BY"
                    /tissue_type="Lens"
                    /dev_stage="Adult"
                    /lab_host="EMDH10B"
                    /note="Organ: Eye; Vector: pCMVSPORT6; Two human lenses
                    from different adults (both approximately 40 years old)
                    together yielded 20ug of total RNA and 150ng mRNA for cDNA
                    library synthesis. A directionally cloned cDNA library in
                    the pCMVSPORT6 vector was constructed at Life Technologies
                    , essentially following the protocols of the SuperScript
                    Plasmid System full details of which are contained in the
                    manufacturer's instruction manual
                    (http://www.lifetech.com/). First strand synthesis was
                    carried out using a Not I primer-adapter
                    (5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCC(T)15-3'). Not I/blunt
                    end inserts were cloned into the Not I/EcoR v sites in the
                    vector. EST analysis was performed on the unamplified
                    library at the NIH Intramural Sequencing Center (NISC)."
BASE COUNT    157 a    112 c    138 g    123 t
ORIGIN
```

Query Match   24.9%; Score 473; DB 12; Length 530;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 473; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy       1406 GCACAGCACCTGCACGAACACCCCGCCCAAACTGTCGGAGGACACCGTGTACAGGAGCGG 1465
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCACAGCACCTGCACGAACACCCCGCCCAAACTGTCGGAGGACACCGTGTACAGGAGCGG 60

Qy       1466 GTTGATGACCGAGCTGAGGTAGAAAAACGTCTCCGAGAAGGGGAGGAGGATCATGTACGC 1525
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 24

```
LOCUS       AL538562                   920 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL538562 LTI_FL013_FBrn1 Homo sapiens cDNA clone CS0DF024Y004 5'
            prime, mRNA sequence.
ACCESSION   AL538562
VERSION     AL538562.1  GI:12866967
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 920)
AUTHORS     Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
    source          1..920
                    /organism="Homo sapiens"
                    /db_xref="taxon:9606"
                    /clone="CS0DF024Y004"
                    /clone_lib="LTI_FL013_FBrn1"
                    /dev_stage="pooled tissue from post conception fetuses (20
                    week, 24 week and 26 week)"
                    /lab_host="DH10B"
                    /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
                    cDNA was primed with a NotI-oligo(dT) primer Five prime
                    end enriched, double-stranded cDNA was digested with Not I
                    and cloned into the Not I and Eco RV sites of the
                    pCMVSPORT 6 vector. Library was constructed by Life
                    Technologies.  Contact : Feng Liang Life Technologies, a
                    division of Invitrogen 9800 Medical Center Drive Rockville
                    , Maryland 20850, USA Fax : (1) 301 610 8371 Email :
                    fliang@lifetech.com URL :
                    http://fulllength.invitrogen.com"
BASE COUNT    172 a    285 c    257 g    199 t    7 others
ORIGIN
```

Query Match   24.9%; Score 472; DB 9; Length 920;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 472; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy         61 GTTGATGACCGAGCTGAGGTAGAAAAACGTCTCCGAGAAGGGGAGGAGGATCATGTACGC 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1526 CCGGAAGTAGGAGACCTCGTCCAGTGCGTGCGTGCTTGGGTTGGCCGCAGAAATGCGGAAT 1585

Qy        121 CCGGAAGTAGGAGACCTCGTCCAGTGCGTGCGTGCTTGGGTTGGCCGCAGAAATGCGGAAT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1586 CTGGGTTGGGGCATCCAGCACCGCCCAATGTCACAACAATCAGCCGCAGAGACACGAGC 1645

Qy        181 CTGGGTTGGGGCATCCAGCATCACGGCCAATGTCACAACAATCAGCCGCAGAGACACGAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1646 AGGAGGGGAGGAGACAGAGAGAAAAACACACCATGAGAACACAGTAAATGAATAAAACC 1705

Qy        241 AGGAGGGGAGGAGACAGAGAGAAAAACACACCATGAGAACACAGTAAATGAATAAAACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1706 ATAAAAATATTTAGGCCCCTCGTTGTTCGTGCTTACTGGCCCAGGAAAATGGTACCAATTTTTCA 1765

Qy        301 ATAAAAATATTTAGGCCCCTCGTTGTTCGTGCTTACTGGCCCAGGAAAATGGTACCAATTTTTCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1766 GTGTTGGACTTGACAGCTTCTTTTGCCACAAGCAAGAGAGAGAATTTAACACTGTTTCAAAC 1825

Qy        361 GTGTTGGACTTGACAGCTTCTTTTGCCACAAGCAAGAGAGAGAATTTAACACTGTTTCAAAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1826 CCGGGGGAGTTGGCTGTGTTAAAGAAAGACCATTAAAATGCTTTAGACAGTGTA 1878

Qy        421 CCGGGGGAGTTGGCTGTGTTAAAGAAAGACCATTAAAATGCTTTAGACAGTGTA 473
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
```

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Qy    155 GCCCCAGCAGCCTCGGCAGCCAGCCACCAGCCTGCAGCCGCAGCCGCAGCCGCAGCCTGCTTCGGCTTGCTGTCGCC 214
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    154 GCCCCAGCAGCCCTCGGCACTCAGCCACCAGCCGCGTGCACCAGCCGGGGCCAGCCGCAGCCTGCTTCCGCTCGCC 213

Qy    215 TCCTTCTGATGCGGCTTGCCCTCTCCCGGGACTCCGGAGAATGTGGGTGCTTCCTAGGC 274
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    214 TCCTTCTGATGCGGCTTGCCCTCTCCCGGGACTCCGGAGAATGTGGGTGCTTAGGC 273
```

```
RESULT 25
BQ689033
LOCUS       BQ689033          879 bp      mRNA    linear    EST 15-JUL-2002
AGENCOURT_8063959 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6207625
DEFINITION  5', mRNA sequence.
ACCESSION   BQ689033
VERSION     BQ689033.1  GI:21814349
KEYWORDS    EST.
SOURCE      human.
 ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 879)
AUTHORS     National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE       NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2364  row: a  column: 02
            High quality sequence stop: 555.
FEATURES             Location/Qualifiers
     source          1..879
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6207625"
                     /clone_lib="NIH_MGC_110"
                     /tissue_type="ductal carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
```

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BASE COUNT      203 a      260 c      241 g      175 t
ORIGIN
```

```
Qy    275 ATCCGGCAACTTTTTGCGGATTGTTCTTGCTTCCAGGCTTTGCCGTCAAATCCAGTGC 334
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274 ATCCGGCAACTTTTTTGCGGATTGTTCTTTGCCTTCCGGCTTTGCCGTCAAATCCAGTGC 333

Qy    335 TACCAGTGTGAAGAAATTCCAGCTCGACTGCTCCTCTCCCCGAGTTCATTGTGAAT 394
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    334 TACCAGTGTGAAGAAATTCCAGCTCGACTGCTCCTCTCCCCGAGTTCATTGTGAAT 393

Qy    395 TGCACGGTGAAGCGTTCAAGACACATGTGTTCAGAAGAAAGAAAGTGCCCGGGATC 454
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394 TGCACGGTGAAGCGTTCAAGACACATGTGTTCAGAAGAAAGTGAAAGTGCCCGGGATC 453

Qy    455 ATGTACCCGCAAGTCCTGTGTCACATCAATCAGGGGGGCGCCTCTCCCGGGGTACCAG 514
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    454 ATGTACCCGCAAGTCCTGTGTCATCATCAGGGGGGCGCCTCTCCCGGGGTACCAG 513

Qy    515 TCCTTCTTCGCTCCTCCCAGGGAAAACTGAACTCAGTTTGCATCAGTCGGGCAACACCCCTCTT 574
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    514 TCCTTCTTCGCTCCTCCCAGGGAAAACTGAACTCAGTTTGCATCAGTCTGCAACACACCCCTCTT 573

Qy    575 TGTAACGGGCCAAGGCCCAAGAAAGAAAAGGGGAAGTTCTGCCTCGGCCCTCAGGC 626
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    574 TGTAACGGGCCAAGGCCCAAGAAAGAAAAGGGGAAGTTCTGCCTCGGCCCTCAGGC 625
```

```
RESULT 26
AI336858
AI336858/c
LOCUS       AI336858          515 bp      mRNA    linear    EST 15-FEB-1999
qx86g11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2009444 3', mRNA
DEFINITION  similar to SW:NTR1_RAT P20789 NEUROTENSIN RECEPTOR TYPE 1 ;, mRNA
            sequence.
ACCESSION   AI336858
VERSION     AI336858.1  GI:4073785
KEYWORDS    EST.
SOURCE      human.
 ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 515)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
```

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Query Match            24.8%;   Score 471;  DB 14;  Length 879;
Best Local Similarity  99.8%;   Pred. No. 0;
Matches  521; Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;
```

```
Qy    871 TGACTGAATTTCAGTATGTACTTGAAGGAAGGAAGGTGGAGTGGAAAGTTCACCCCATGT 930
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    22 TGACTGAATTTCAGTATGTACTTGAAGGAAGGAAGGTGGAGTGGAAAGTTCACCCCATGT 81

Qy    931 CTGTGTAACCGGAGTCAAGGCCAGGCTGGCAGAGTCWGTCCTTGAGAGTCACTGAGGTGG 990
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    82 CTGTGTAACCGGAGTCAAGGCCAGGCTGGCAGAGTCACTGAGTCCTTGAGAGTCACTGAGGTGG 141

Qy    991 GCATCTCCCTTTTTGTAAAGCCTCCCAGTGTCCCATTCCATCCCTGAATGGGGGCATAGTTGA 1050
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   142 GCATCTGCCTTTTGTAAAGCCTCCCAGTGTCCATTCCATCCCTGATGGGGGCATAGTTGA 201

Qy   1051 GACTGCAGAGTGAGAGTGACAGTTTTTCTTAGGGGTGGAGGGGCAGTTCCCACTCAAGGCTC 1110
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   202 GACTGCAGAGTGAGAGTGACAGTTTTTCTTAGGGGTGGAGGGGCAGTTCCCACTCAAGGCTC 261

Qy   1111 CCTCGGCTTGACATTCAAACTTCATGCTCCTCGAAAAACCATTCTCTGCACCAGAATTGGCTG 1170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   262 CCTCGGCTTGACATTCAAACTTCATGCTCCTGAAAAACCATTCTCTGCACCAGAATTGGCTG 321

Qy   1171 GTTTTCCGGCCTGAGTTGGGCTCTTAGTGACTCCAGACTCAAATGACTGGGACTTAGACTGGG 1230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   322 GTTTTCCGGCCTGAGTTGGGCTCTTAGTGACTCCAGACTCAAATGACTGGGACTTAGACTGGG 381

Qy   1231 GCTCGGCCCTCGCTCTGAAAAGTTGGCTTAAGAAAAATCTTCAGTTCTCCTTGGCAGGAGGACT 1290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   382 GCTCGGCCCTCGCTCTGAAAAGTTGGCTTAAGAAAAATCTTCAGTTCTCCTTGCCAGGAGGACT 441

Qy   1291 GGCGCCGGGAGCCGAAGACAACGGGGGCGCTGCACAAAGCGGCGCTCGGTGGTGGAGT 1350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   442 GGCGCCGGGAGCCGAAGACAACGGGGGCGCTGCACAAAGCGGCGCTCGGTGGTGGAGT 501

Qy   1351 GCGCAGCATGTACCGGCAGGCGCGTTCTCTGGTTGGGCGTGCTGCA 1392
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   502 GCGCAGCATGTACCGGCAGGCGCTTCTCTGGTTGGGCGTGCTGCA 543
```

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                 Clone distribution: NCI-CGAP clone distribution information can be
                 found through the I.M.A.G.E. Consortium/LLNL at:
                 www-bio.llnl.gov/bbrp/image/image.html
                 High quality sequence stop: 444.
                 Seq primer: -40UP from Gibco
                 Insert Length: 1161   Std Error: 0.00

FEATURES         Location/Qualifiers
     source      1..515
                 /organism="Homo sapiens"
                 /db_xref="taxon:9606"
                 /clone="IMAGE:2009444"
                 /clone_lib="NCI_CGAP_GC6"
                 /tissue_type="pooled germ cell tumors"
                 /lab_host="DH10B"
                 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                 polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
                 from the normalized library NCI_CGAP_GC4 was prepared, and
                 ss circles were made in vitro. Following HAP purification,
                 this DNA was used as tracer in a subtractive hybridization
                 reaction. The driver was PCR-amplified cDNAs from a pool
                 of 5,000 clones made from the same library (cloneIDs
                 1257096-1258631, 1469064-1470983, and 1475592-1476743).
                 Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       103 a      142 c      119 g      151 t
ORIGIN

Query Match              24.5%;      Score 464;   DB 9;   Length 515;
Best Local Similarity    99.8%;
Matches   514;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy  1367  GCGCTTCTCGGTGGTTGGGTTGGGGCGTTGCTTGCTCCAGCGGCCACCTGCACGAACAC  1426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   515  GCGCTTCTCGGTGGTTGGGTTGGGGCGTTGCTTGCTCCAGCGGCCACCTGCACGAACAC   456

Qy  1427  CCGGCGAAACTGCTGCCAGGACACCGTGTCAGCAGGAGCTGAGGTTGATGACCGAGGTA  1486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   455  CCGGCGAAACTGCTGCCAGGACACCGTGTCAGCAGGAGCTGAGGTTGATGACCGAGGTA   396

Qy  1487  GAAAAACGTCTCCGAGAAGGGGGAGGAGGATCATGTACGCCGGAAGTAGGACCTCGTCCA  1546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   395  GAAAAACGTCTCCGAGAAGGGGGAGGAGGATCATGTACGCCCGGAAGTAGGACCTGTCCA   336

Qy  1547  GTCGTGCTTGGGTTTGGGTTTGGGGCCCAGCCACATGGCTTGGGCATCCAGCATAC  1606
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   335  GTCGTGCTTGGGTTTGGGTTTGGGGCCCAGCCAATCTGGTTGGGCATCCAGCATAC   276

Qy  1607  GGCCAATGTCACACAATCAGCCCTGGGCAGCACGGCAGGGAGGAGACAGAGAAAA  1666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   275  GGCCAATGTCACACAATCAGCCCTGGGCAGCACGGCAGGGAGGAGACAGAGAAAA   216

Qy  1667  GAAAAACACAGCATGAGACACAGTAAATGAATAAAACCATAAAATATTTAGCCCCTCTG  1726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   215  GAAAAACACAGCATGAGACACAGTAAATAAAATAATTTAGCCCCTCTG            156

Qy  1727  TTCTCTGCTTACTGTGCCCAGAAAATGGTACCAATTTTTCAGTGTTGACTTGACAGCTTCT  1786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   155  TTCTGTGCTTACTGTGCCAATTTTTCAGTGTTGACTTGACAGCTTCT              96

Qy  1787  TTTTGCCACAAGCAAGAGAGAATTTAACACGTGTTTCAAAACCCGGGGGAGTTGGCTGTGTTA  1846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    95  TTTTGCCACAAGCAAGAGAGAATTTAACACGTGTTTCAAAACCCGGGGGAGTTGGCTGTGTTA   36

Qy  1847  AAGAAGAGACCATTAAATGCTTTAGACAGTGTAAAA  1881
          ||||||||||||||||||||||||||||||||
Db    35  AAGAAGAGACCATTAAATGCTTTAGACAGTGTAAAA  1
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ACCESSION      AW149665
VERSION        AW149665.1   GI:6197561
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1  (bases 1 to 690)
AUTHORS        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE          National Cancer Institute, Cancer Genome Anatomy Project
               (CGAP/BTGAP), Tumor Gene Index
JOURNAL        Unpublished (1998)
COMMENT        Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               Tissue Procurement: Burt Feuerstein, M.D., Mark Israel, M.D.
               cDNA Library Preparation: M. Bento Soares, Ph.D.
               cDNA Library Arrayed by: Greg Lennon, Ph.D.
               DNA Sequencing by: Washington University Genome Sequencing Center
               Clone distribution: NCI-CGAP clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               www-bio.llnl.gov/bbrp/image/image.html
               Possible reversed clone: similarity on wrong strand
               Seq primer: -40UP from Gibco
               High quality sequence stop: 402.

FEATURES       Location/Qualifiers
     source    1..690
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="IMAGE:2620569"
               /clone_lib="NCI_CGAP_Brn50"
               /tissue_type="medulloblastoma"
               /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
               modified polylinker (phage resistant)"
               /lab_host="DH10B (phage resistant)"
               modified polylinker; 1st strand cDNA was prepared from a
               medulloblastoma tumor tissue, and was then primed with a
               Not I - oligo(dT) primer. Double-stranded cDNA was ligated
               to Eco RI adaptors (Pharmacia), digested with Not I and
               cloned into the Not I and Eco RI sites of the modified
               pT7T3 vector. This library is normalized. Library
               constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT     142 a      196 c      160 g      191 t      1 others
ORIGIN

Query Match              23.48%;     Score 444;   DB 10;   Length 690;
Best Local Similarity    99.5%;
Matches   594;  Conservative   0;  Mismatches   3;  Indels   0;  Gaps   0;

Qy  1282  CAGAGGACTGGCCCGGAGACGGAGAAGAGAGCAACGGGCGTGCACAAAGCCGTGTCGG  1341
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   607  CAGAGGACTGGCCCGGAGACGGAGAAGAGAGCAACGGGCGTGCACAAAGCCGTGTCGG   548

Qy  1342  TGGTGGAGTGCGCATGTACGCGCCGGAGCCGCTTCGTGGTTGGGGTGCAGGAGGC  1401
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   547  TGGTGGAGTGCGCATGTACGCGCCGGAGCCGCTTCGTGGTTGGGGTGCAGGAGGC   488

Qy  1402  GGCAGCACAGCCACCTGCACGAACACCCGCCGAAACTGCTGCGAGGACACGTGTACGAGGA  1461
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   487  GGCAGCACAGCCACCTGCACGAACACCCGCCGAAACTGCTGCGAGGACACCGTGTACGAGGA   428

Qy  1462  GCCGGTTGATGACCGAGCTGAGGTAGAAAAACGTCTCCGAGAAGGGGGAGGAGGATCATGT  1521
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   427  GCCGGTTGATGACCGAGCTGAGGTAGAAAAACGTCTCCGAGAAGGGGGAGGAGGATCATGT   368

Qy  1522  ACGCCCGGAAGTAGGACCTGTCCAGTCGTGCTTGGGTTTGGGTTTGGGGCCCAGCCATCC  1581
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   367  ACGCCCGGAAGTAGGACCTCGTCCAGTCGTGCTTGGGTTTGGGTTTGGGGCCCAGCCATCC   308

Qy  1582  GAATCTGGTTGGGCATCCAGCATACGGCCAATGTCACAACAATCAGCCCTGGGCAGACAC  1641
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   307  GAATCTGGTTGGGCATCCAGCATACGGCCAATGTCACAACAATCAGCCCTGGGCAGACAC   248
```

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Qy   1642 GAGCAGGAGGGAGAGAGAGAAAAGAAAAACACAGCCATGAGAACACAGTAAATGAATAA 1701
          ||||| || ||| |||||||||||||| | ||||||||||||||||||| || ||||||
Db    247 GAGCAGAAGGAGAGAGAAAAGAAAAACACAGCACCATGAGAACACAGTAAATAAATAA 188

Qy   1702 AACCATAAAATATTTAGCCCCTCTGTTCTCGTGCTTACTGGCCAGGAAATGGTACCAATTT 1761
          ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||| |||
Db    187 AACCATAAAATATTTAGCCCCTCTGTTCTCGTGCTTACTGGCCAGGAAATGGTACCAATTT 128

Qy   1762 TTCAGTGTTGGACTTGACAGCTTCTTTTTGCCACAACGACAGAGAATTAACACTGTTTC 1821
          |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 TTCAGTGTTGGACTTGACAGCTTCTTTTTGCCACAACGACAGAGAATTAACACTGTTTC 68

Qy   1822 AAACCCGGGGAGTTGGCGTGTTGTTAAAGAAAGACCATTAAATGCTTTAGACAGTGTA 1878
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     67 AAACCCGGGGAGTTGGCGTGTTGTTAAAGAAAGACCATTAAATGCTTTAGACAGTGTTTC 11
```

RESULT 28

LOCUS   BM667957/c

BM667957   538 bp   mRNA   linear   EST 27-FEB-2002
DEFINITION UI-E-DW0-agm-j-01-0-UI.s1 UI-E-DW0 Homo sapiens cDNA clone
            UI-E-DW0-agm-j-01-0-UI 3', mRNA sequence.
ACCESSION   BM667957
VERSION   BM667957.1 GI:18975788
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 538)
AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE   Normalization and subtraction: two approaches to facilitate gene
            discovery
JOURNAL   Genome Res. 6 (9), 791-806 (1996)
MEDLINE   97044477
COMMENT   Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES   Location/Qualifiers
     source   1..538
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="UI-E-DW0-agm-j-01-0-UI"
                     /clone_lib="UI-E-DW0"
                     /tissue_type="lens"
                     /dev_stage="adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-DW0 is a cDNA library containing the following
                     tissue(s): lens. The library was constructed according to
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. First strand cDNA synthesis was primed with an
                     oligo-dT primer containing a Not I site. Double stranded
                     cDNA was ligated to an EcoR I adaptor, digested with Not
                     I, and cloned directionally into pT7T3-Pac vector. The
                     oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is CGATTAGCGA. This library
                     was created for the program, Gene Discovery in the Visual

```
Qy   1405 AGCACAGCACCTGCCACGAACACCCCGCCGAAAACTGCTTGCGAGGAGGACACCGTGTACGTACG 1524
          || ||| |||| ||| |||||||||||||| |||||||||||||||||||||||||||||||
Db    431 GGTTGATGACCGACGCTGAGGTAGAAAAAAGTCTCCGAGAAGGGGAGGAGGATCATGTACG 372

Qy   1465 GGTTGATGACCGAGCGTGAGGTAGAAAAAAAGTCTCCGAGAAGGGGAGGAGGACACGCGAGG 1524
```

RESULT 29

LOCUS   AW075598/c

AW075598   500 bp   mRNA   linear   EST 13-OCT-1999
DEFINITION xb24e07.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:2577252 3'
            similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
            GPR39.; , mRNA sequence.
ACCESSION   AW075598
VERSION   AW075598.1 GI:6030596
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 500)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgaps-r@mail.nih.gov
            Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
            Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
            I.M.A.G.E. Consortium cDNA Sequencing by: Washington University
            Genome Sequencing Center

BASE COUNT   104 a   144 c   122 g   167 t   1 others
ORIGIN
Query Match   23.2%; Score 440; DB 13; Length 538;
Best Local Similarity   99.8%; Pred. No. 0;
Matches 490; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

FEATURES   Location/Qualifiers
    source   1..500
                  /organism="Homo sapiens"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:2577252"
                  /clone_lib="NCI_CGAP_Kid13"
                  /tissue_type="2 pooled Wilms' tumors, one primary and one
                  metastatic to brain"
                  /lab_host="DH10B"
                  /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: SalI;
                  Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                  Library constructed by Life Technologies."

BASE COUNT   99 a   139 c   114 g   148 t
ORIGIN

High quality sequence stop: 413.
Seq_primer: -40UP from Gibco
Possible reversed clone: similarity on wrong strand

Query Match   23.1%; Score 439; DB 10; Length 500;
Best Local Similarity   99.8%;
Matches   489; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1389 TGCACGGACAGGCGGCCAGCACAGCACACCTGCAGGAACACCGCCCGGAAACTGCTGCAGGAC 1448
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   490 TGCACGGACAGGCGGCCAGCACAGCACCTGCACGGAACACCGCCCGGAAACTGCTGCCGAGGAC 431

Qy   1449 ACCGTGCTACAGGAGCCGCGGGGTTGATGACCGAGCGTGAGGTAGAAAAAAACGTCTCCGAGGAAGGGG 1508
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   430 ACCGTGCTACAGGAGCGGCGGGTTGATGACCGAGCGTGAGGTAGAAAAAACGTCTCCGAGGAAGGGG 371

Qy   1509 AGGAGGGATCATGTACGGCCCCGGAAGTAGGAACCTGCGTCCAGTGCGTGCTTGGGGTTTGGCCGGCA 1568
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   370 AGGAGGGATCATGTACGGCCCCGGAAGTAGGAACCTGCGTCCAGTGCGTGCTTGGGGTTTGGCCGGCA 311

Qy   1569 GCCATGCATCCTCCGGAATCTGGTTGGGCCATCCAGCATACGGCCAAGTCACAACAATCAGC 1628
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   310 GCCATGAATCCTCCGGAATCTGGTTGGGCCATCCAGCATACGGCCAAGTCACAACAATCAGC 251

Qy   1629 CCTGGGCAGACGACGGAGCGAGGAGAGAGAGAGAAAAGAGAAAAACACAGACATGAGAACAC 1688
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   250 CCTGGGCAGACGACGGAGCGAGGAGAGAGAAAAGAGAAAAACACAGACATGAGAACAC 191

Qy   1689 AGTAAATGAATAAAAACCATAAAAATATTTAGCCCCTCTGTTGTCTGTGCTTACTGGCCAGGAA 1748
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   190 AGTAAATAAATAAAAACCATAAAAATATTTAGCCCCTCTGTTGTCTGTGCTTACTGGCCAGGAA 131

Qy   1749 ATGGTACCAATTTTCAGTGTTGGACTTGACAGCTTCTTTTGCCACAAGCAAGAGAGAGAAT 1808
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   130 ATGGTACCAATTTTCAGTGTTGGACTTGACAGCTTCTTTTGCCACAAGCAAGAGAGAGAAT 71

Qy   1809 TTAACACTGTTTCAAACCCGGGGGGAGTTGGCTGTGTGTTAAAGAAAGACCATTAAATGCTTT 1868
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   70 TTAACACTGTTTCAAACCCGGGGGAGTTGGCTGTGTGTTAAAGAAAGACCATTAAATGCTTT 11

Qy   1869 AGACAGTGTA 1878
           ||||||||||
Db   10 AGACAGTGTA 1

RESULT 30
BE731003
BE731003
LOCUS   BE731003   794 bp   mRNA   linear   EST 15-SEP-2000
DEFINITION 601570968P1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845440 5',
            mRNA sequence.
ACCESSION   BE731003
VERSION   BE731003.1 GI:10144995
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens

REFERENCE   1 (bases 1 to 794)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM543 row: h column: 17
            High quality sequence stop: 642.

FEATURES   Location/Qualifiers
    source   1..794
                  /organism="Homo sapiens"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:3845440"
                  /clone_lib="NIH_MGC_21"
                  /tissue_type="choriocarcinoma"
                  /lab_host="DH10B (phage-resistant)"
                  /note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
                  Site_2: EcoRI; cDNA made by oligo-dT priming.
                  Directionally cloned into EcoRI/XhoI sites using the
                  following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                  for average insert size 1.8kb. Library constructed by
                  Ling Hong in the laboratory of Gerald M. Rubin (University
                  of California, Berkeley) using ZAP-cDNA synthesis kit
                  (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT   195 a   227 c   217 g   155 t
ORIGIN

Query Match   22.5%; Score 426; DB 12; Length 794;
Best Local Similarity   100.0%;
Matches   426; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   26 GGGCCCGGGAGGCGCGGGGAGCGGGGAGGGGAGCAGAGAACCCGGAGCCAGCCGGCGGGGGGCCA 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GGGCCCGGGGAGGCGCGGGGAGCGGGGAGGGGAGCAGAGAACCCGGAGCCAGCCGGCGGGGGGCCA 60

Qy   86 TGCAGGCTCCGCGAGACGGCGCACCTGCGGCGCTCCTCTAAGCTTACGAGCGTCGCTCCGCGGCA 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TGCAGGCTCCGCGAGACGGCGCACCTGCGGCGCTCCTCTAAGCTTACGAGCGTCGCTCCGCGGCA 60

Qy   146 GCAGCGCGGCGGGGCCCCAGCAGCCTCGGCACCCACACGCCGTGCAGCCGCCGGCAGCCTCCCGCT 205
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GCACGCGCGGCGGGGCCCCCAGCACCCCTCGGCACCCACACGCCGTGCAGCCGCCGGCAGCCTCCGCT 180

Qy   206 GCTGTCGCCTCCTCTGATCGCCGCTTGCCCTCTCCCGGCGGACTCCGGGAGAAATGTGG 265
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GCTGTCGCCTCCTCTGATCGCCGCTTGCCCTCTCCCGGCGGACTCCGGGAGAAATGTGG 240

Qy   266 GTCCTAGGCATCGGCGCAACTTTTTGCGGATTGTTTTCTTGCTTCCAGGCTTTGCGCGTGCAA 325
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GTCCTAGGCATCGGCGCAACTTTTTGCGGATTGTTTTCTTGCTTCCAGGCTTTGCGCGTGCAA 300

Qy   326 ATCCAGTGCTTACCAGTGTGAAGAAATTCAGCTGAACAACGAGACTGCTTCCTCCCCCGAGTTC 385
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 ATCCAGTGCTACCAGTGTGAAGAAATTCAGCTGAACAACGAGACTGCTTCCTCCCCCGAGTTC 360

Qy   386 ATTGTGAAATTGCACGGTGAAGCGTTCAAGACATGTGTCAGAAAGAAAGTGAATGGACGAAAGT 445
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATTGTGAAATTGCACGGTGAAGCGTTCAAGACATGTGTCAGAAAGAAAGTGAATGGACGAAAGT 420

Qy   446 GCCGGG 451
           ||||||
Db   421 GCCGGG 426

RESULT 31

```
LOCUS       BE730800                1134 bp    mRNA    linear   EST 15-SEP-2000
DEFINITION  601570755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845557 5',
            mRNA sequence.
ACCESSION   BE730800
VERSION     BE730800.1  GI:10144792
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1134)
  AUTHORS   NIH-MGC http://mgc.nci.nlm.nih.gov/,
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgaps-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM543 row: m column: 14
            High quality sequence stop: 640.
FEATURES             Location/Qualifiers
     source          1..1134
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3845557"
                     /clone_lib="NIH_MGC_21"
                     /tissue_type="choriocarcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin
                     (University of California, Berkeley) using ZAP-cDNA
                     synthesis kit (Stratagene) and Superscript II RT (Life
                     Technologies)."
BASE COUNT      329 a    320 c    308 g    177 t
ORIGIN
```

Query Match   22.5%; Score 426; DB 12; Length 1134;
Best Local Similarity   100.0%;
Matches 426; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy     26 GGCCCGGGAGCCGCAGCCGGAGAGCAGAGACCCGCACCGGAGCCCGGGACGCCGGGCGA 85
          ||||||||||||||||| ||| |||||||||||||||||||||||||||||||||||| ||
Db      1 GGCCCGGGAGCCGCAGGCGGGAGGCAGAGACCCGCACCGGAGCCCGGGACGCCGGGCGGGA 60

Qy     86 TGCAGGCGTCCCGCGAGCGGCCACCTGCGCGGGCGTCTCTAAGCTACGACCGTCTCCGCGG 145
          |||||||||||||||||||||||||||||||| ||| |  ||||||||||||||| || |
Db     61 TGCAGGCGTCCCGCGAGCGGCCACCTGCGCGGCGTCCCCTAAGCTACGACCGTCGCGGCA 120

Qy    146 GCAGGCGGGGCCCCAGGGCCCAGAGCCTCGGAGACCACAGCGTGCACGGCTGCAGCCTCGGT 205
          ||||| ||| ||| || |||||||| || ||| |||||| | | |  ||||||||||||||
Db    121 GCAGGCGGGGCCCCACGAGCCCAGACCCGTCGCAGCCCGCCTGCGCCGGGGCAGCCTCCGGT 180

Qy    206 GCTGTGTCGCCTCCTTCTGATGCGCGTTGCCCTCTGGGCCCCGGGGGGACTCGGGAGAAATGTGG 265
          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db    181 GCTGTGTCGCCTCCTTCTGATGCGCGTTGCCCTCTCCGGGCCCCGGGGGACTCGGGAGAAATGTGG 240

Qy    266 GTCCTAGGCCATCGCGGCGCAACTTTTTGCGGATTGTTCTTGCTTCCAGGCTTTCGCCTGCAA 325
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GTCCTAGGCCATCGCGGCGCAACTTTTTGCGGATTGTTCTTGCTTCCAGGCTTTCGCCTGCAA 300

Qy    326 ATCCAGTGCTACCAGTGTGAAGAATTCCAGTGAACAAACGACTGCTGTCCCCCGAGTTC 385
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ATCCAGTGCTACCAGTGTGAAGAATTCCAGTGAACAAACGACTGCTGTCCCCCGAGTTC 360

Qy    386 ATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTCAGAAAGAAGTGATGGAGCAAAGT 445
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTCAGAAAGAAGTGATGGAGCAAAGT 420

Qy    446 GCCGGG 451
          ||||||
Db    421 GCCGGG 426
```

RESULT 32

AI150931/c

```
LOCUS       AI150931                 467 bp    mRNA    linear   EST 26-OCT-1998
DEFINITION  qb53c04.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1703814 3',
            similar to SW:NTR1_RAT P20789 NEUROTENSIN RECEPTOR TYPE 1 ;, mRNA
            sequence.
ACCESSION   AI150931
VERSION     AI150931.1  GI:3679400
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 467)
  AUTHORS   NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTGAP), Tumor Gene Index
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D.,
            Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1149  Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 425.
FEATURES             Location/Qualifiers
     source          1..467
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1703814"
                     /clone_lib="NCI_CGAP_Brn23"
                     /tissue_type="glioblastoma (pooled)"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGACGGCGCCACCATATCTTTTTTTTTTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pT7T3 vector.
                     Library is normalized, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT      106 a    119 c     92 g    150 t
ORIGIN
```

Query Match   22.4%; Score 425; DB 9; Length 467;
Best Local Similarity   100.0%;
Matches 425; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy   1454 GTACAGGACGCGGGGTTGATGACCGAGCTGAGGTAGAAAAACGTCTCCGAGAGGAGGAG 1513
          |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    467 GTACAGGAGCGGGGTTGATGACCGAGCTGAGGTAGAAAAACGTCTCCGAGAGGAGGAG 408

Qy   1514 GATCATGTACGGCCCGGAAGTAGGACCTCGTCGTTGCTTGGGTTTGGGCCGCAGCCAT 1573
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    407 GATCATGTACGGCCCGGAAGTAGGACCTCGTCGTTGCTTGGGTTTGGGCCGCAGCCAT 348
```

RESULT 33

```
Qy   1574 GATCCTTCCGAATCTCGAGTTGGGTTGGGCATCCAGCATACGGCCAATGTCACAACAATCAGCCCTGG 1633
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    347 GATCCTTCCGAATCTCGGTTGGGCATCCAGCATACGGCCAATGTCACAACAATCAGCCCTGG 288

Qy   1634 GCAGACACCGAGCGAGGAGGAGGAGGAGGAGCAGACACACGCATGAGAACACAGTAA 1693
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    287 GCAGACACCGAGCGAGGAGGAGGAGGAGGAGCAGACACACGCATGAGAACACAGTAA 228

Qy   1694 ATGAATAAAAACCATTAAAAATATTTAGCCCCTCTGTTCTGTTCTACTGGCCAGGAAAATGGT 1753
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    227 ATGAATAAAAACCATTAAAAATATTTAGCCCCTCTGTTCTGTTCTACTGGCCAGGAAAATGGT 168

Qy   1754 ACCAATTTTTCAGTGTGTTGGACTTGACAGCTTCTTTTTGCCACAACGAAGAGAGAGAATTTAAC 1813
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    167 ACCAATTTTTCAGTGTGTTGGACTTGACAGCTTCTTTTTGCCACAACGAAGAGAGAGAATTTAAC 108

Qy   1814 ACTGTTTCAAACCCGGGGGAGTTGGCTGTCGTGTTAAAGAAAAGACCATTAAAATGCCTTTAGACA 1873
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    107 ACTGTTTCAAACCCGGGGGAGTTGGCTGTCGTGTTAAAGAAAAGACCATTAAAATGCCTTTAGACA 48

Qy   1874 GTGTA 1878
          |||||
Db     47 GTGTA 43
```

LOCUS   BE336607   480 bp   mRNA   linear   EST 14-JUL-2000
DEFINITION bb68e04.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030654 5', mRNA
           sequence.
ACCESSION   BE336607
VERSION   BE336607.1 GI:9189000
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 480)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Other_ESTs: bb68e04.x1
           Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: DCID/DTP
           cDNA Library Preparation: Ling Hong/Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Washington University Genome Sequencing Center
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           Image.llnl.gov/image/html/iresources.shtml
           Seq primer: -40RP from Gibco
           High quality sequence stop: 449.
FEATURES   Location/Qualifiers
     source   1..480
           /organism="Homo sapiens"
           /db_xref="taxon:9606"
           /clone="IMAGE:3030654"
           /clone_lib="NIH_MGC_9"
           /tissue_type="adenocarcinoma cell line"
           /lab_host="DH10B (phage-resistant)"
           /note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
           EcoRI; cDNA made by oligo-dT priming. Directionally
           cloned into EcoRI/XhoI sites using the following 5'
           adaptor: GGCACGAG(G). Size-selected >500bp for average
           insert size 1.8kb. Library constructed by Ling Hong in
           the laboratory of Gerald M. Rubin (University of
           California, Berkeley) using ZAP-cDNA synthesis kit
           (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT   86 a   154 c   153 g   87 t
ORIGIN

Query Match   22.4%;   Score 425;   DB 10;   Length 480;

Best Local Similarity 99.8%; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Matches 475; Conservative 0; Mismatches 0; Pred. No. 0; Indels 0; Gaps 0;

```
Qy      1 GCCAACTCCGGAGAGGCYCTGGTGCTCCGGCCCGCCGAGCGGAGCGGAGGAGGAGACCCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCCAACTCCGGAGAGGCTCTGGTGCTCCGGCCCGCCGAGCGGAGCGGAGGAGGAGACCCG 60

Qy     61 CAGCCGGGGAGCCCGGCGGCGGATGCAGCCGGGCGGATCGGCTCCGAGCGGCGCTCCTCTA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CAGCCGGGGAGCCCGGCGGCGGATGCAGCCGGGCGGATCGGCTCCGAGCGGCGCTCCTCTA 120

Qy    121 AGCTACCGACCGTGTCTCCGCGGCGCAGCAGCCGGGCGCCCCAGGCCTGGCGCCACAGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGCTACCGACCGTGTCTCCGCGGCGCAGCAGCCGGGCGCCCCAGGCCTGGCGCCACAGC 180

Qy    181 CGGCTGCAGGCCAGCCGCAGCCTCGCGTCGCTGTCGCTCCTCTCTGATGCGGTGCTTCCCG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CGGCTGCAGGCCAGCCGCAGCCTCGCGTCGCTGTCGCTCCTCTCTGATGCGGTGCTTCCCG 240

Qy    241 GCCCCGGGACTCGGGAGGAAATGTGGGTCCTAGGCACATCGGGCAACTTTTTGCGGATTGTT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GCCCCGGGACTCGGGAGGAAATGTGGGTCCTAGGCACATCGGGCAACTTTTTGCGGATTGTT 300

Qy    301 CTTGCTTCCAGGCGTTTGGGCGTGCAAATCCAGTGGTGAAGGAATTCCAGCTGAA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTTGCTTCCAGGCGTTTGGGCGTGCAAATCCAGTGGTGAAGGAATTCCAGCTGAA 360

Qy    361 CAACGACTGCCTCCTCCCCCGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACACATG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAACGACTGCCTCCTCCCCCGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACACATG 420

Qy    421 TCAGAAAGAAGTGATGGAGCAAAGTGCCGGGGATCATGTACCGGCCAAGTGCCTGTGCAT 476
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TGAGAAAGAAGTGATGGAGCAAAGTGCCGGGGATCATGTACCGGCCAAGTGCCTGTGCAT 476
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RESULT 34

LOCUS   BF126050   759 bp   mRNA   linear   EST 24-OCT-2000
DEFINITION 601762888F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026092 5',
           mRNA sequence.
ACCESSION   BF126050
VERSION   BF126050.1 GI:10965090
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 759)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: ATCC/DCTD/DTP
           cDNA Library Preparation: Ling Hong/Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
           Plate: LLCM855 row: o column: 21
           High quality sequence stop: 723.
FEATURES   Location/Qualifiers
     source   1..759
           /organism="Homo sapiens"
           /db_xref="taxon:9606"
           /clone="IMAGE:4026092"
           /clone_lib="NIH_MGC_20"
           /tissue_type="melanotic melanoma"
           /lab_host="DH10B (phage-resistant)"
           /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
           EcoRI; cDNA made by oligo-dT priming. Directionally
           cloned into EcoRI/XhoI sites using the following 5'

RESULT 35

```
BF125134
LOCUS       BF125134       843 bp    mRNA    linear    EST 24-OCT-2000
DEFINITION  601762356F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4025340 5',
            mRNA sequence.
ACCESSION   BF125134
VERSION     BF125134.1  GI:1096174
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 843)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
  COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM853  row: p  column: 13
            High quality sequence stop: 711.
FEATURES             Location/Qualifiers
     source          1..843
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Query Match            22.4%;  Score 424;  DB 12;  Length 759;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches  424;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1186 TGGGCTCTTAGTGACTCGAGACTCAAATGACTGGGACTTAGACTGGGGCTTCGGCCTCGCTCT 1245
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      76 TGGGCTCTTAGTGACTCGAGACTCAAATGACTGGGACTTAGACTGGGGCTTCGGCCTCGCTCT 135

Qy    1246 GAAAAGTGCTTAAGAAAAATCTTCTCAGTTCTCCTTGCAGAGGACTGGGCGCCGGGGACGGCGA 1305
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     136 GAAAAGTGCTTAAGAAAAATCTTCTCAGTTCTCCTTGCAGAGGACTGGGCGCCGGGGACGGCGA 195

Qy    1306 AGAGCAACGGGCGCCTGCACAAAACGGGGCGCCTGTTCGGTTGGTGGTGGAGTGGCGCCCA 1365
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     196 AGAGCAACGGGCGCCTGCACAAAACGGGGCGCCTGTTCGGTTGGTGGTGGAGTGGCGCCCA 255

Qy    1366 GGGCGCTTCTCGTGTTGGCGTGCTGCCGACAGGGCGCCGCAGCACCTGCACGAACA 1425
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     256 GGGCGCTTCTCGTGTTGGCGTGCTGCCGACAGGGCGCCGCAGCACCTGCACGAACA 315

Qy    1426 CCCGCCGAAAACTGCTCGGAGGACACCGTGTACAGGAGGACCGGGTTGATGACCGAGCTGAGGT 1485
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     316 CCCGCCGAAAACTGCTCGGAGGACACCGTGTACAGGAGGACCGGGTTGATGACCGAGCTGAGGT 375

Qy    1486 AGAAAAAACGTCTCCGAGAAGGGGGAGGGGGGATCATGTACGCCCGGAAAGTAGGACCTCGTCC 1545
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     376 AGAAAAAACGTCTCCGAGAAGGGGGAGGGGGGATCATGTACGCCCGGAAAGTAGGACCTCGTCC 435

Qy    1546 AGTCGTGCTTGCTTGGGTTTGGCCGCAGCCCATGATCTCCGAAATCTGGTTGGGCATCCAGCATA 1605
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     436 AGTCGTGCTTGCTTGGGTTTGGCCGCAGCCCATGATCTCCGAAATCTGGTTGGGCATCCAGCATA 495

Qy    1606 CGGC 1609
           ||||
Db     496 CGGC 499
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RESULT 36

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BM709964
LOCUS       BM709964       571 bp    mRNA    linear    EST 28-FEB-2002
DEFINITION  UI-E-CQ1-agc-c-21-0-UI.r1 UI-E-CQ1 Homo sapiens cDNA clone
            UI-E-CQ1-agc-c-21-0-UI 5', mRNA sequence.
ACCESSION   BM709964
VERSION     BM709964.1  GI:19023222
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
  COMMENT   Contact: Soares, MB
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Query Match            22.4%;  Score 424;  DB 12;  Length 843;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches  424;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1186 TGGGCTCTTAGTGACTCGAGACTCAAATGACTGGGACTTAGACTGGGGCTTCGGCCTCGCTCT 1245
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      76 TGGGCTCTTAGTGACTCGAGACTCAAATGACTGGGACTTAGACTGGGGCTTCGGCCTCGCTCT 135

Qy    1246 GAAAAGTGCTTAAGAAAAATCTTCTCAGTTCTCCTTGCAGAGGACTGGGCGCCGGGGACGGCGA 1305
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     136 GAAAAGTGCTTAAGAAAAATCTTCTCAGTTCTCCTTGCAGAGGACTGGGCGCCGGGGACGGCGA 195

Qy    1306 AGAGCAACGGGCGCCTGCACAAAACGGGGCGCCTGTTCGGTTGGTGGTGGAGTGGCGCCCA 1365
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     196 AGAGCAACGGGCGCCTGCACAAAACGGGGCGCCTGTTCGGTTGGTGGTGGAGTGGCGCCCA 255

Qy    1366 GGGCGCTTCTCGTGTTGGCGTGCTGCCGACAGGGCGCCGCAGCACCTGCACGAACA 1425
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     256 GGGCGCTTCTCGTGTTGGCGTGCTGCCGACAGGGCGCCGCAGCACCTGCACGAACA 315

Qy    1426 CCCGCCGAAAACTGCTCGGAGGACACCGTGTACAGGAGGACCGGGTTGATGACCGAGCTGAGGT 1485
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     316 CCCGCCGAAAACTGCTCGGAGGACACCGTGTACAGGAGGACCGGGTTGATGACCGAGCTGAGGT 375

Qy    1486 AGAAAAAACGTCTCCGAGAAGGGGGAGGGGGGATCATGTACGCCCGGAAAGTAGGACCTCGTCC 1545
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     376 AGAAAAAACGTCTCCGAGAAGGGGGAGGGGGGATCATGTACGCCCGGAAAGTAGGACCTCGTCC 435

Qy    1546 AGTCGTGCTTGCTTGGGTTTGGCCGCAGCCCATGATCTCCGAAATCTGGTTGGGCATCCAGCATA 1605
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     436 AGTCGTGCTTGCTTGGGTTTGGCCGCAGCCCATGATCTCCGAAATCTGGTTGGGCATCCAGCATA 495

Qy    1606 CGGC 1609
           ||||
Db     496 CGGC 499
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BASE COUNT      225 a    192 c    255 g    171 t
ORIGIN

FEATURES             Location/Qualifiers
     source          1..843
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4025340"
                     /clone_lib="NIH_MGC_20"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
                     /lab_host="DH10B (phage-resistant)"
                     /tissue_type="melanotic melanoma"
```

Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.

FEATURES   Location/Qualifiers
     source   1..571
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="UI-E-CQ1-agc-c-21-0-UI"
                     /clone_lib="UI-E-CQ1"
                     /tissue_type="optic nerve"
                     /dev_stage="adult"
                     /lab_host="DH10B (life Technologies) (T1 phage resistant)"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-CQ1 is a normalized cDNA library containing the
                     following tissue(s): optic nerve. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     CCATTAAGTC. This library was created for the program, Gene
                     Discovery in the Visual System, supported by National Eye
                     Institute (NEI)."
BASE COUNT   189 a   170 c   109 g   3 others
ORIGIN

Query Match
Best Local Similarity   22.3%;
Matches 423; Conservative 0;

Qy   19 GGTGCTTCGGCCCGGGAGCCGGGAGCGAAGACAACCCGGAGCCCCCAGCG 78
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   15 GGTGCTTCGGCCCGGGAGCCGGGAGCGAAGACAACCCGGAGCCCCCAGCG 74

Qy   79 CGGGGCAATGCAGGGCTCCGCGAGGCGACCCGCTCCTCTAAGCTACGACCGTCGTCTC 138
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   75 CGGGGCGATGCAGGGCTCCGCGAGGCGACCCGTCCTCTAAGCTACGACCGTCGTCTC 134

Qy 139 CGCGGCCAGCAGCGCGGGCGCCCCAGAGCACCAGCGCGCTGCAGCGCCCAGC 198
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 135 CGCGGCAGCACGCGGGCGCCCCAGCACCTCGGCACCACGGCTGCAGCCGGCAGC 194

Qy 199 CTCCGGCTGCTGTCGCCTCGCCTTGCCTCTCCCGGGGGACTCCGGGAG 258
        |||||||||||||||||||||||||||||||||||||||||||||||
Db 195 CTCCGGCTGCTGTCGCCTCCTCCTGATGCGGCTCCCCTTCCCCGGGGGACTCCGGGAG 254

Qy 259 AATGTGGGTCCTTAGGCATCGCGCCGCAACTTTTTTGCGGATTGTTCTTGCTTCAGGCTTTGC 318
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 255 AATGTGGGTCCTTAGGCATCGCGCCGCAACTTTTTTGCGGATTGTTCTTGCTTCAGGCTTTGC 314

Qy 319 GCTGCAAATCCAGTGCTGTGTGAAGAAATTCCAGCTGTGAACAACGAACTGCTTCGTCTCCC 378
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 315 GCTGCAAATCCAGTGCTGTCACCAGTGTGAACAACGACTGCTTCAGGCGTTGC 374

Qy 379 CGAGTTCATTGTGAATTGCACGGTGAACGTTCAGAAAGAAGTGATGGA 438
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db 375 CGAGTTCATTGTGAATTGCACGGTGAACGTTCAGAAAGAAGTGATGGA 434

Qy 439 GCA 441
        |||
Db 435 GCA 437

RESULT 37

LOCUS   AI018769   537 bp   mRNA   linear   EST 27-AUG-1998
DEFINITION ov32e04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639038
            3', similar to SW:NTR1_RAT P20789 NEUROTENSIN RECEPTOR TYPE 1 ;;
            mRNA sequence.
ACCESSION   AI018769
VERSION   AI018769.1 GI:3232567
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 537)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
            , Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1394 Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 452.
FEATURES   Location/Qualifiers
     source   1..537
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from mRNA obtained from Clontech Laboratories
                     , Inc., and primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATTCGAAGTGGGACGCGCGCGCCCAAATTTTTTTTTTTTTTT 3'].
                     Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization to Cot5, and was
                     constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT   105 a   147 c   126 g   159 t
ORIGIN

Query Match
Best Local Similarity   21.9%;
Matches 515; Conservative 0;

Qy 1354 CATGTACGCGCACGAGCGCCGGCCGTTCTCTCGGGTTGGGTTGGCGTTGGCGTTGCAGCGACGACGACAGCA 1413
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 537 CATGTACGCGCACGAGCGCCGCTTCTCGTGGTTGGGCGTTGGCGTTGCAGCGACGACGACGACAGCA 478

Qy 1414 CCTGCACGAACACCCGCCCGAAACTGCTGGAGGACACGCGTACAGGAGGCGGGTTGATGA 1473
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 477 CCTGCACGAACACCCGCCGAAACTGCTGGAGGACACGCGTACAGGAGGCGGGTTGATGA 418

Qy 1474 CCGAGCTGAGGTAGAAAAACGTCTCCGAGAAGGGGAGGATCATGTACGCCCGGAAGT 1533
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 417 CCGAGCTGAGGTAGAAAAACGTCTCCGAGAAGGGGAGGATCATGTACGCCCGGAAGT 358

Qy 1534 AGGACCTCGTCCAGTCGTGCTTGGGTTCGGCCCGCAGCCAATGATCCTCCGAATCTCGGTTGG 1593

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Db    357  AGGACCTCGTCCAGTCGTCGTTGGGTTTGGCCCAGCCATTGATCCTCCGAATCTGGTTGG
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1594  GCATCCAGCATACGGCCAATGTCACAACAATCAGCCCTGGGCACAGCAGGAGGGA 1653
Db    297  GCATCCAGCATACGGCCAATGTCACAACAATCAGCCCTGGGCACAGCAGGAGGGA 298

Qy   1654  GAGACAGAGAAAAGAAAACACACAGCCATGAGACAACAGTAAATGAATAAAAACCATAAAATA 1713
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    237  GAGACAGAGAAAAGAAAACACACAGCCATGAGACAACAGTAAATGAATAAAAACCATAAAATA 178

Qy   1714  TTTAGCCCCTCTCGTTCTCGTTGCTTACTGGGCCAGAAATGGTACCAATTTTTCAGTGTTGGA 1773
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    177  TTTAGCCCCTCTCGTTCTCGTTGCTTACTGGGCCAGAAATGGTACCAATTTTTCAGTGTTGGA 118

Qy   1774  CTTGACAGCTTCTTTTGCCACAAGACAAGAGAGAAATTTAACACTGTTTCAAACCCGGGGGGA 1833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    117  CTTGACAGCTTCTTTTGCCACAAGACAAGAGAGAAATTTAACACTGTTTCAAACCCGGGGGGA 58

Qy   1834  GTTGGCTGTGTTGTTAAAGAAAGAAGACCATTAAATGCTTTAG 1870
           |||||||||||||||||||||||||||||||||||||||||||
Db     57  GTTGGCTGTGTTGTTAAAGAAAGAAGACCATTAAATGCTTTAG 21
```

```
RESULT 38
BI544761
LOCUS       BI544761              688 bp    mRNA    linear   EST 05-SEP-2001
DEFINITION  603242028F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5284638 5',
            mRNA sequence.
ACCESSION   BI544761
VERSION     BI544761.1  GI:15432073
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 688)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11719  row: g  column: 07
            High quality sequence stop: 688.
FEATURES             Location/Qualifiers
     source          1..688
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5284638"
                     /clone_lib="NIH_MGC_95"
                     /tissue_type="hippocampus"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTVN-3',
                     size-selected for average insert size 2.5 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for full-length clones and constructed using the
                     Cap-trapper method (Carninci, in preparation) Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT  123 a  223 c  223 g  119 t
ORIGIN
Query Match   21.5%;  Score 408;  DB 13;  Length 688;
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Best Local Similarity 100.0%; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 408; Conservative 0; Pred. No. 0;

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Qy     19  GGTGCTCGGCCCGGGCCGGGAGCGGCGGGAGGAGGAGGACCCGGCGGGAGCCCGGACGG 78
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194  GGTGCTCGGCCCGGGCCGGGAGCGGCGGGAGGAGGAGGACCCGGCGGGAGCCCGGACGG 253

Qy     79  CGGGCGGATGCAGGCTCGGCGACCGGCGACCTCGGGCGTCGGCGTCCTCTAAGCCTACGAGCGTCGTGCTC 138
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    254  CGGGCGGATGCAGGCTCGGCGACCGGCGACCTCGGGCGTCGGCGTCCTCTAAGCCTACGAGCGTCGTGCTC 313

Qy    139  CGCGGCAGCACGCGCGGGCGCCCCAGCGGCCTCGCCAGCGCGGCAGC 198
           |||||||||||||||||||||||||||||||||||||||||||||||
Db    314  CGCGGCAGCACGCGCGGGCGCCCCAGCGGCCTCGCCAGCGCGGCAGC 373

Qy    199  CTCCGCTGCTCGTGCGCCTCCTCTGATCGCCTTGCCCCGGGGACTCCGGGAG 258
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374  CTCCGCTGCTCGTGCGCCTCCTCTGATCGCCTTGCCCCGGGGACTCCGGGAG 433

Qy    259  AATGTGGGTCCTAGGCATCGCGGCCAACTTTTTTGCGGATTGTTGTCTTCCAGGCTTTGC 318
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    434  AATGTGGGTCCTAGGCATCGCGGCCAACTTTTTTGCGGATTGTTGTCTTCCAGGCTTTGC 493

Qy    319  GCTGCAAAATCCAGTGCTACCAGTGTGAGAAGAAATTCCAGCTGAACAACGACTGCTCCTCCCC 378
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    494  GCTGCAAAATCCAGTGCTACCAGTGTGAGAAGAAATTCCAGCTGAACAACGACTGCTCCTCCCC 553

Qy    379  CGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTCAGAA 426
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db    554  CGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTGTCAGAA 601
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RESULT 39
BI669845
LOCUS       BI669845              690 bp    mRNA    linear   EST 12-SEP-2001
DEFINITION  603293440F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5312889 5',
            mRNA sequence.
ACCESSION   BI669845
VERSION     BI669845.1  GI:15584078
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 690)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11792  row: p  column: 10
            High quality sequence stop: 690.
FEATURES             Location/Qualifiers
     source          1..690
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5312889"
                     /clone_lib="NIH_MGC_96"
                     /tissue_type="hypothalamus"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3',
                     size-selected for average insert size 2.3 kb and
                     normalized to ROT 5. This is a primary library enriched
```

RESULT 40

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LOCUS       BE395797                 743 bp    mRNA    linear   EST 21-JUL-2000
DEFINITION  601310028F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631543 5',
            mRNA sequence.
ACCESSION   BE395797
VERSION     BE395797.1  GI:9341162
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 743)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM321  row: h  column: 08
            High quality sequence stop: 600.
FEATURES             Location/Qualifiers
     source          1..743
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3631543"
                     /clone_lib="NIH_MGC_44"
                     /tissue_type="endometrium, adenocarcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Library constructed by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT     127 a     231 c     202 g     130 t
ORIGIN
```

```
Query Match        99.8%;  Score 408;  DB 13;  Length 690;
Best Local Similarity   99.8%;
Matches  648;  Conservative  0;  Pred. No.  0;  Mismatches  0;  Indels  2;  Gaps  2;

Qy    19  GGTGCTTCGGCCCCGGGAGCCCGAGCGGGAGGAGAGACCCGCAGCCCGGCGAGGCCCGAGCG   78
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    42  GGTGCTTCGGCCCCGGGAGCCCGAGCGGGAGGAGAGACCCGCAGCCCGGCGAGGCCCGAGCG  101

Qy    79  CGGGCGGATGCAGCAGGCTCCCCGGAGCGGAGCGCACCTGCGGCCTCCTCTAAGCTACCACC  138
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   102  CGGGCGGATGCAGCAGGCTCCCCGGAGCGGAGCGCACCTGCGGCCTCCTCTAAGCTACCACC  161

Qy   139  CGGGGCGAGCAGCGGGGGGGGGGGGGGGCGGCGCAGCCTCGGCAGCCTGCAGGACCGTGCTCT  198
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   162  CGGGGCGAGCAGCGGGGGGGCCCAGCCTCGGCAGCCTGCAGCCGCCGGGGGCAGC  221

Qy   199  CTCCGCTGCGTGTCGCCTCCTCTGATGCGGCGTTAGCCGCCTCCCTCTCCGGGGACTCCGGGAG  258
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   222  CTCCGGCTGCTGTCGCCTCCTCTGATGCGGCTGCCCTCTCCGGGGACTCCGGGAG  281

Qy   259  AATGTGGGTGCCTCCTAGGCATGCGGCGGAACTTTTTTGCGGGATTGTGTTCTTTGCTTCCAGGCTTTGC  318
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   282  AATGTGGGTGCCTAGGCATCGCGGCGCAACTTTTTTGCGGATTGTGTTCTTTGCTT-CAGGCTTTGC  340

Qy   319  GCTGGCAAATCCAGTGCTACCA-GTGTGAAGAATTCCAGCTGAACAACGACTGCTCCTCCC  377
          ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db   341  GCTGCAAATCCCAGTGCTACCAGGTGTGAAGAATTCCAGCTGAACAACGACTGCTCCTCCC  400

Qy   378  CCGAGTTCATTGTGAATTGCACGTGTCAAGACATGTGTCGAGAAAGAAGTGATGG  437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   401  CCGAGTTCATTGTGAATTGCACGGTGTCAAGACATGTGTCAAGAAAGAAGTGATGG  460

Qy   438  AGCAAAAGTGCCGGGATCATCATGTACCCCGCCAAGTGTCCTGTGCCATCATCACGGGCGGCCTGTGTCTCCATCG  497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   461  AGCAAAAGTGCCGGGATCATCATGTACCCCGCCAAGTGTCCTGTGCCATCATCACGGGCGGCCTGTGTCTCCATCG  520

Qy   498  CCTCTCGCCGGGTACAGTCCTTCTCCTCCCCAGGGAAACTGAACCTCAGTTTTGCATCAGCT  557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   521  CCTCTGTCCGGGGTACCAGTCGTCTTCTCCTCCCCAGGGAAACTGAACCTCAGTTTGCATCAGCT  580

Qy   558  GCTGCAACACCCCTCTTTGTTAACGGGGCCCAAGAGAAAAGGGGGAAGTTCTGCCTCGG  617
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   581  GCTGCAACACCCCTCTTTGTTAACGGGCCAAGAGAAAAGGGGAAGTTCTGCCTCGG  640

Qy   618  CCCTCAGGGCCAGGGTCCGGCAACCACCACCATCCTGTTCCTCAAATTAGCCCTC  667
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   641  CCCTCAGGGCCAGGGCTCCGCAACACCACCATCCTGTTCCTCAAATTAGCCCTC  690
```

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BASE COUNT     160 a     189 c     214 g     180 t
ORIGIN

Query Match        99.6%;  Score 404;  DB 10;  Length 743;
Best Local Similarity   99.6%;
Matches  504;  Conservative  0;  Pred. No.  0;  Mismatches  2;  Indels  0;  Gaps  0;

Qy   752  CTGAGTGAGTTTCTTCTTCTCGGGTGTGGTGTCCTTTTATTCTGGGTTAGGGAGGCGGGAGTTCGGTTGTTCT  811
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    65  CTGAGTGAGTTTCTTCTTCTGGGTGTCCTTTTATTCTGGGTTAGGGAGGCGGGAGTTCGGTTGTTCT  124

Qy   812  CTTTTGTTCCCTGTGCAAATAATGAAAAGAGCTCGGTAAAGCCATTCTGAATAAATTCAGCYT  871
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   125  CTTTTGTTCCCTGTGCAAATAATGAAAAGAGCTCGGTAAAGCCATTCTGAATAAATTCAGCCT  184

Qy   872  GACTGAATTTCAGTATGTCACTTGAAGGAAGGAGGTGGGAAGAGTTCACCCCATGTC  931
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   185  GACTGAATTTCAGTATGTACTTGAAGGAAGGAGGGTGGGAAGTTCACCCCATGTC  244

Qy   932  TGTGTAACCGGAGTCAAGGCCCAGGCTGGCAGAGTCWGTCCTTAGAAGTCACTCAAGGTGG  991
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   245  TGTGTAACCGGAGTCAAGGCCAGGCTGGCAGAGTCAGTCCTTAGAAGTCACTGAGGTGG  304

Qy   992  CATCTGCCTTTTGTAAAGCCTCCAGTGTCCATTCCATCCCTGATGGGGGCATAGTTTGAG  1051
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   305  CATCTGCCTTTTGTAAAGCCTCCAGTGTCCATTCCATCCCTGATGGGGCATAGTTTGAG  364

Qy  1052  ACTGCAGAGTGAGAGTGAGTTTTCTTAGGGCTTGGGAGGGCCAGTGTTCCCACTCAAGGCTCC  1111
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   365  ACTGCAGAGTGAGAGTGAGAGTTTTCTTAGGGCTGGGAGGGCCAGTGTTCCCACTCAAGGCTCC  424

Qy  1112  CTCGCTTGACATTTCAAAACTTCAGTGCTCCTGAAAAACCATTCTCTGCCAGCAGAAGTTGGCTGG  1171
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   425  CTCGCTTGACATTTCAAAACTTCATCGCTCCTGAAAAACCATTCTCTGCCAGCAGAAGTTGGCTGG  484

Qy  1172  TTTCGCGCCTGAGTTGGCGTCTAGTGACTCGGAGACTCAAATGACTGGGACTTAGACTTGGGG  1231
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   485  TTTCGCGCCTGAGTTGGCGTCTAGTGACTCGGAGACTCAAATGACTGGGACTTAGACTTGGGG  544

Qy  1232  CTCGGCCCTCGCTCTGAAAAAGTGCTTA  1257
          ||||||||||||||||||||||||||||
Db   545  CTCGGCCCTCGCTCTGAAAAGTGCTTA  570
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RESULT 41

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LOCUS       AA613995                 396 bp    mRNA    linear   EST 06-OCT-1997
DEFINITION  no86c08.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1113710 3',
            mRNA sequence.
ACCESSION   AA613995
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```
ACCESSION   AA613995
VERSION     AA613995.1  GI:2466129
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 396)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Stratagene, Inc., David B. Krizman,
            Ph.D.
            cDNA Library Arraying: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 395.
FEATURES             Location/Qualifiers
     source          1..396
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1113710"
                     /clone_lib="NCI_CGAP_AA1"
                     /tissue_type="adrenal adenoma"
                     /note="Organ: adrenal gland; Vector: Bluescript SK-;
                     /lab_host="SOLR (kanamycin resistant)"
                     Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally.
                     Primer: Oligo dT. Two pooled bulk adrenal adenomas. 5'
                     adaptor sequence: 5' GAATTCGGCACGAG 3' 3' adaptor
                     sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTTT 3' Average insert
                     size: 1.6 kb."
BASE COUNT      135 a    103 c    102 t
ORIGIN       56 a    135 c    103 g    102 t

Query Match     Best Local Similarity   100.0%;
Matches 396;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
                        Score 396;  DB 9;  Length 396;
                        Pred. No. 0;

Qy   1296 CGGGACCGGAAGCAACGGGGCGCCTGCACAAAGCGGCGGCCTGTCGGTGGTGTGGAGTGCGCCA 1355
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    396 CGGGACCGGAAGCAACGGGGCGCCTGCACAAAGCGGCGGCCTGTCGGTGGTGTGGAGTGCGCCA  337

Qy   1356 TGTACCGCGCAGCGCGCTTCTCGTGGTTGGCGTCGCTGCAGCGACAGGCGGCGCAGACACAGACC 1415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    336 TGTACCGCGCAGCGCGCTTCTCGTGGTTGGCGTCGCTGCAGCGACAGGCGGCGCAGACACAGACC  277

Qy   1416 TGCACGACGAACACCCGCGAAACTGCTCGCAGGAGCGACACCGTGTACAGGAGCGGGTTGATGACC 1475
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    276 TGCACGACGAACACCCGCGAAACTGCTCGCAGGAGCGACACCGTGTACAGGAGCGGGTTGATGACC  217

Qy   1476 GAGCTGAGGTAGAAAAAACGTCTCCGAGAAGGGGAGGAGGGGAGGAGGACACCGTGTACGCCCGGAAGTAG 1535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    216 GAGCTGAGGTAGAAAAAACGTCTCCGAGAAGGGGAGGAGGGGAGGAGGATCATGTACGCCCGGAAGTAG  157

Qy   1536 GACCTGTCCAGTCGTCGTTGGGTTTGGCCCGCAGCCATGATCTCCGAATCTGGTTGGGC 1595
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    156 GACCTGTCCAGTCGTCGTTGGGTTTGGCCCGCAGCCATGATCTCCGAATCTGGTTGGGC   97

Qy   1596 ATCCAGCATACGGCCAATGTCACACAACAAATCAGCCCTTCGGCAGACACGGAGAGGGAGA 1655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     96 ATCCACCATACGGCCAATGTCACAACAATCAGCCCTTCGGCACACGGAGAGGGGAGA   37

Qy   1656 GACAGAGAAAAAGAAAAAACACAGCATGAGAACACAGT 1691
          ||||||||||||||||||||||||||||||||||||||
Db     36 GACAGAGAAAAAGAAAAAACAGCAGCATGAGAACACAGT    1
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RESULT 42
AI391683/c
LOCUS       AI391683                 452 bp    mRNA    linear    EST 17-MAR-1999
DEFINITION  qy93f04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2019583 3',
            mRNA
            sequence.
            similar to SW:NTR1_RAT P20789 NEUROTENSIN RECEPTOR TYPE 1 ;, mRNA
            sequence
ACCESSION   AI391683
VERSION     AI391683.1  GI:4217687
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 452)
  AUTHORS   NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTGAP), Tumor Gene Index
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
            Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1183   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 451.
FEATURES             Location/Qualifiers
     source          1..452
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2019583"
                     /clone_lib="NCI_CGAP_Brn25"
                     /tissue_type="anaplastic oligodendroglioma"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCGGCCGCANAGGTTTTTTTTTTTTTTTTTT
                     T 3'];  double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pT7T3 vector.
                     Library is normalized, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT       94 a    122 c     99 g    137 t
ORIGIN

Query Match     Best Local Similarity   99.8%;
Matches 444;  Conservative 0;  Mismatches 0;  Indels 1;  Gaps 0;
                        Score 394;  DB 9;  Length 452;
                        Pred. No. 0;

Qy   1433 AAACTGCTCGCAGGAGCACCGTGTACAGGAGCGGGTTGATGACCGAGCTGAGGTAGAAAAA 1492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    445 AAACTGCTCGCAGGAGCACCGTGTACAGGAGCGGGTTGATGACCGAGCTGAGGTAGAAAAA  386

Qy   1493 CGTCTCCGAGAAGGGGAGGAGGGGAGGAGGATCATGTACGCCCGGAAGTAGGACCTGTCCAGTCGTCGTG 1552
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db    385 CGTCTCCGAGAAGGGGAGGAGGGGAGGAGGATCATGTACGCCCGGAAGTAGGACCTGTCCAGTCGTCGTG  326

Qy   1553 CTTGGGTTTGGCCCGCAGCCATGATCCTCCGAAATCTGGTTGGGCATCCAGCATACGGCCAAT 1612
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    325 CTTGGGTTTGGCCCGCAGCCATGATCCTCCGAAATCTGGTTGGGCATCCAGCATACGGCCAA  266

Qy   1613 TGTCACAACAATCAGCCCTGGGCACACGAGCACGAGGGAGAGGACAGAGAAAAAGAAAAAA 1672
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    325 CTTGGGTTTGGCCCGCAGCCATGATCCTCCGAAATCTGGTTGGGCATCCAGCATACGGCCAA  266
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Db   265 TGTCACAACAATCAGCCCTGGGCAGACGAGCAGGAGGAGAGACAGAGGAAAAGAAAA 206
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1673 CACAGACATGAGAACACAGTAAATGAATAAAAACCATAAAATATTTAGCCCTCTGTTCTGT 1732
         |||||||||||||||||||||||| ||||||||||||||||||||||||||||| |||||
Db   205 CACAGACATGAGAACACAGTAAATAAATAAAAACCATAAAATATTTAGCCCTCTGTCTGT 146
Qy  1733 GCTTACTGCCCAGAAAATGGTACCAAATTTTTCAGTGTTGGACTTGACAGCTTCTTTTGCC 1792
         |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   145 GCTTACTGCCCAGGAAAATGGTACCAAATTTTTCAGTGTTGGACTTGACAGCTTCTTTTGCC 86
Qy  1793 ACAAGACAAGAGAGAATTTAACACTGTTTCAAACCCGGGGGGAGTTGGCTGTGTTAAAGAAA 1852
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    85 ACAAGACAAGAGAGAATTTAACACTGTTTCAAACCCGGGGGGAGTTGGCTGTGTTAAAGAAA 26
Qy  1853 GACCATTAAATGCTTTAGACAGTGT 1877
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RESULT 43
LOCUS   AI499630/c   396 bp   mRNA   linear   EST 12-MAY-1999
DEFINITION to03b07.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2177941 3'
            similar to SW:NTR1_RAT P20789 NEUROTENSIN RECEPTOR TYPE 1 ;, mRNA
            sequence.
ACCESSION   AI499630
VERSION   AI499630.1 GI:4391612
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 396)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40UP from Gibco
            Insert Length: 826 Std Error: 0.00
            High quality sequence stop: 395
            POLYA=NO.
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:2177941"
                     /clone_lib="NCI_CGAP_Ut2"
                     /tissue_type="moderately-differentiated endometrial
                     adenocarcinoma, 3 pooled tumors"
                     /lab_host="DH10B"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.85 kb. Life Technologies catalog #:
                     11539-012"
BASE COUNT   62 a   124 c   96 g   114 t
ORIGIN

Qy 1328 GCGGGCGCTGTCGCTGGTGGTGGAGTGGCGCCATGATACGCCACAGGCCGCTTCTGGGTTGGCGGTG 1387
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Query Match        20.6%;  Score 390;  DB 9;  Length 396;
Best Local Similarity   100.0%;
Matches  390;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Db   396 GCGGGCGCTGTCGCTGGTGGTGGAGTGGCGCCATGATACGCCACAGGCCGCTTCTGGGTTGGCGGTG 337
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Qy  1388 CTGCAGCGGACAGGCCAGCCAGCACACAGCACGACGCCTGCACACACACACCCCGGGAAACTGCTGCGAGGA 1447
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   336 CTGCAGCGGACAGGCCAGCCAGCACACAGCACGACGCCTGCACACACACACCCCGGGAAACTGCTGCGAGGA 277
Qy  1448 CACCGTGTACAGGAGGCGGGGTTGATGACCGAGCGTAGAAAAACCTCTCCGAGGAAGGG 1507
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   276 CACCGTGTACAGGAGGCGGGGTTGATGACCGAGCGTAGAAAAACCTCTCCGAGGAAGGG 217
Qy  1508 GAGGAGGATCATGTACGCCCCGGGAAGTAGGACCTCGCCCCAGTCGTCGTCGTTGGGCCGC 1567
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   216 GAGGAGGATCATGTACGCCCCGGGAAGTAGGACCTCGCCCCAGTCGTCGTCGTTGGGCCGC 157
Qy  1568 AGCCATGAGTCCTCCGAAATCTGGTTGGGCCATCCAGCATACGGCCAAATGTCACAACAATCAG 1627
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Db   156 AGCCATGAGTCCTCCGAAATCTGGTTGGGCCATCCAGCATACGGCCAAATGTCACAACAATCAG 97
Qy  1628 CCCTGGGCAGACACGAGCACGAGGAGGAGAGACAGAGGAAAAGAAAACACAGCATGAGAACA 1687
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Db    96 CCCTGGGCAGACACGAGCACGAGGAGGAGAGACAGAGGAAAAGAAAACACAGCATGAGAACA 37
Qy  1688 CAGTAAATGAATAAAACCATAAAATATTTA 1717
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Db    36 CAGTAAATGAATAAAACCATAAAATATTTA 7
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RESULT 44
LOCUS   BE746601   654 bp   mRNA   linear   EST 15-SEP-2000
DEFINITION 601580186F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928868 5',
            mRNA sequence.
ACCESSION   BE746601
VERSION   BE746601.1 GI:10160593
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 654)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM760 row:1 column: 21
            High quality sequence stop: 651.
FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_9"
                     /tissue_type="adenocarcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies),"
BASE COUNT   121 a   219 c   187 g   126 t   1 others
ORIGIN
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Query Match           20.2%;    Score 383;  DB 12;  Length 654;
Best Local Similarity  99.8%;   Pred. No. 0;
Matches 503; Conservative   0; Mismatches   0; Indels  1; Gaps  1;

Qy   29 CCGGGGAGCCGAGCGGGGAGGAGAGAGAGCAGAGACCCGGGAGCCCGAGCGCCGGGCGGATGC 88
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Db    4 CCGGGGAGCCGAGCGGGGAGGAGAGAGAGCAGAGACCCGGGAGCCCGAGCGCCGGGCGGATGC 63

Qy   89 AGGCTCCCGGAGGGGCACCTGCGGCGCTCCTCTCAAGCTACGACCGTCGTCGTCCGCGGCAGCA 148
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64 AGGCTCCCGGAGGGGCACCTGCGGCGCTCCTCTCAAGCTACGACCGTCGTCGTCCGCGGCAGCA 123

Qy  149 GCCGGGGCCCCAGCAGCCACCAGCCCGGGGCCAGCAGCCCAGCCTCGCGCTGCT 208
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  124 GCCGGGGCCCCAGCAGCCACCAGCCCGGGGCCAGCAGCCCAGCCTCGCGCTGCT 183

Qy  209 GTCGCCCTCCTCTGATGCGCTTGCCCTCTTCTCCCGGCCCCCGGGGACTCCGGGAGAATGTGGGTC 268
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  184 GTCGCCCTCCTCTGATGCGCTTGCCCTCTTCTCCCGGCCCCCGGGGACTCCGGGAGAATGTGGGTC 243

Qy  269 CTAGGCANTCGCGCGCAACTTTTTTGCGGATTGTTGTTCTTGCTTCCCAGCGCTTTGCGCTGCAAA-T 327
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db  244 CTAGGCANTCGCGCGCAACTTTTTTGCGGATTGTTGTTCTTGCTTTGCGCTCCAAACT 303

Qy  328 CCAGTGCTCACCAGTGTGAAGAATTCCAGCTGAACAACGACTGCTCTCCCCCCCGAGTTCAT 387
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Db  304 CCAGTGCTCACCAGTGTGAAGAATTCCAGCTGAACAACGACTGCTCTCCCCCCCGAGTTCAT 363

Qy  388 TGTGAAATTGCACGGTGAACGTTCAAGACAGTATGTGTCAGAGAAAGAAGTGAGTGGACGAAAAGTGC 447
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Db  364 TGTGAAATTGCACGGTGAACGTTCAAGACATGTGTCAGAGAAAGAAGTGAGTGGACAAAAGTGC 423

Qy  448 CGGGATCANTGTACCGGACAAGTCCGTGCATCATCAGCCGGCCTGTTCTCATCGCTCTGCGCGG 507
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Db  424 CGGGATCANTGTACCGGACAAGTCCGTGCATCATCAGCCGGCCTGTTCTCATCGCTCTGCCGG 483

Qy  508 GTACCAGTCCTTTCTGCTCCCCAGG 531
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Db  484 GTACCAGTCCTTTCTGCTCCCCAGG 507


RESULT 45
AI765236/c

LOCUS       AI765236                 456 bp    mRNA     linear   EST 21-DEC-1999
DEFINITION  w172h08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398911 3',
            similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
            GPR39.;, mRNA sequence.
ACCESSION   AI765236
VERSION     AI765236.1   GI:5231745
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 961   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 453.
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                     /clone_lib="NCI_CGAP_Kid12"
                     /lab_host="DH10B"
                     /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     plasmid DNA from the normalized library NCI_CGAP_Kid5 was
                     prepared, and ss circles were made in vitro. Following HAP
                     purification, this DNA was used as tracer in a subtractive
                     hybridization reaction. The driver was PCR-amplified cDNAs
                     from a pool of 5,000 clones made from the same library
                     (cloneIDs 1323912-1325831, 1471368-1472903 and
                     1492104-1493255). Subtraction by Bento Soares and M.
                     Fatima Bonaldo."
BASE COUNT       93 a    122 c     99 g    142 t
ORIGIN


Query Match           20.0%;    Score 380;  DB 9;  Length 456;
Best Local Similarity  99.8%;   Pred. No. 0;
Matches 430; Conservative   0; Mismatches   0; Indels  1; Gaps  0;

Qy 1427 CCGCCGAAAACTGCTGGGAGGACACACCGTTGTACAGGACCGGGGTTGATGACCGAGGTA 1486
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Db  456 CCGCCGAAAACTGCTGGGAGGACACACCGTTGTACAGGACCGGGGTTGATGACCGAGGTA 397

Qy 1487 GAAAAACGTCTCCGAGAAGGGGAGGAGGATCATGTACGGCCCGGAAGTAGGACCTCGTCCA 1546
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  396 GAAAAACGTCTCCGAGAAGGGGAGGAGGATCATGTACGGCCCGGAAGTAGGACCTCGTCCA 337

Qy 1547 GTCGTGCTTGGGTTGGCCCGCAGCCATGATCCTCCGAATCTGTTGGTTGGCCATCCAGCATAC 1606
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  336 GTCGTGCTTGGGTTGGCCCGCAGCCATGATCCTCCGAATCTGTTGGTTGGCCATCCAGCATAC 277

Qy 1607 GGCCAATGTCACAACAATCACCCCTGGGCACGACACCGAGGAGGGAGACAGAGAAAA 1666
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Db  276 GGCCAATGTCACAACAATCAGCCCTGGGCACGACACCGAGGAGGGAGACAGAGAAAA 217

Qy 1667 GAAAAAACACACCATGAGAACACAGTAAATGAATAAAAACCATAAAATATTTAGCCCCTCTG 1726
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  216 GAAAAAACACACCATGAGAACACAGTAAATAAATAAAAACCATAAAATATTTAGCCCCTCTG 157

Qy 1727 TTCTGTGCTTACTGGCCAGGAAATGGTACCAATTTTTCAGTGTTGGACTTGACAGCTTCT 1786
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Db  156 TTCTGTGCTTACTGGCCAGGAAATGGTACCAATTTTTCAGTGTTGGACTTGACAGCTTCT 97

Qy 1787 TTTTGCCACAAGCAGAGAGAGAATTTAACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTTA 1846
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   96 TTTTGCCACAAGCAGAGAGAGAATTTAACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTTA 37

Qy 1847 AAGAAAGACCA 1857
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Job time : 2574.81 secs
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115

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run On: November 7, 2002, 09:53:42 ; Search time 71.0849 Seconds
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Title: US-09-970-966-214
Perfect score: 1897
Sequence: 1 gccaactccggaggctctgg..............aaaaaaaaaaaaaaaaaaa 1897

Scoring table: IDENTITY_NUC
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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	% Query Match	Length	DB	ID	Description
1	56.4	3.0	1872	1	US-08-153-848-39	Sequence 39, Appl
2	56.4	3.0	1872	4	US-09-299-843A-39	Sequence 39, Appl
3	56.4	3.0	1872	4	US-09-088-337B-39	Sequence 39, Appl
c 4	56.4	3.0	1872	5	PCT-US93-11153-39	Sequence 39, Appl
c 5	55.6	2.9	477	1	US-09-135-994-1	Sequence 1, Appl
c 6	55.4	2.9	1028	4	US-08-118-200-1	Sequence 1, Appl
c 7	55.4	2.9	1028	1	US-08-458-745-1	Sequence 1, Appl
c 8	55.4	2.9	10348	4	US-08-457-273B-41	Sequence 41, Appl
c 9	50.8	2.7	10348	3	US-08-556-419-13	Sequence 13, Appl
10	50.8	2.7	10348	1	US-09-041-886-14	Sequence 14, Appl
11	50.8	2.7	10348	1	US-08-246-982A-5	Sequence 5, Appl
12	50.8	2.7	10366	1	US-08-453-265-5	Sequence 5, Appl
13	50.4	2.7	7218	1	US-08-232-463-14	Sequence 14, Appl
14	50.2	2.7	4403765	4	US-09-103-840A-2	Sequence 2, Appl
15	50.2	2.6	4411529	4	US-09-103-840A-1	Sequence 1, Appl
16	50	2.6	6379	1	US-08-499-215-1	Sequence 1, Appl
17	49.4	2.6	7218	1	US-08-232-463-14	Sequence 14, Appl
18	49.2	2.6	4362	2	US-08-455-073A-1	Sequence 1, Appl
19	49.2	2.5	2625	4	US-09-245-041-18	Sequence 18, Appl
20	47.2	2.5	3765	3	US-07-705-490-1	Sequence 1, Appl
21	47.2	2.5	3765	1	US-07-751-891B-1	Sequence 1, Appl
22	47.2	2.5	4072	4	US-09-245-041-16	Sequence 16, Appl
23	47.2	2.5	8569	4	US-09-245-041-14	Sequence 14, Appl
24	47.2	2.5	4403765	4	US-09-103-840A-2	Sequence 2, Appl
25	46.8	2.5	2846	4	US-09-613-182-5	Sequence 5, Appl
26	46.6	2.5	1176	4	US-09-200-090-3	Sequence 3, Appl
27	46	2.4	289	4	US-09-007-005-17	Sequence 17, App
28	46	2.4	289	4	US-09-244-796-17	Sequence 17, Appl
29	45.8	2.4	4362	2	US-08-455-073A-1	Sequence 1, Appl
30	45.6	2.4	1051	4	US-09-245-041-10	Sequence 10, Appl
31	45.6	2.4	1342	3	US-08-832-399-1	Sequence 1, Appl
c 32	45.6	2.4	1342	4	US-09-372-498-1	Sequence 1, Appl
c 33	45.6	2.4	1575	3	US-08-858-876A-1	Sequence 1, Appl
c 34	45.6	2.4	1575	1	US-09-472-880-1	Sequence 1, Appl
c 35	45.6	2.4	2419	4	US-09-245-041-8	Sequence 8, Appl
36	45.6	2.4	3000	4	US-09-236-097-7	Sequence 7, Appl
37	45.6	2.4	8827	2	US-08-460-269c-5	Sequence 5, Appl
38	45.4	2.4	4257	2	US-09-245-041-1	Sequence 1, Appl
39	45.4	2.4	4257	1	US-09-259-821A-1	Sequence 1, Appl
40	45.4	2.4	4257	1	US-08-843-659-1	Sequence 1, Appl
41	45.4	2.4	12001	1	US-08-458-568A-11	Sequence 11, Appl
c 42	44.8	2.4	700	4	US-09-236-097-7	Sequence 7, Appl
c 43	44.8	2.4	1071	2	US-08-997-080-180	Sequence 180, App
c 44	44.8	2.4	1071	2	US-08-997-362-180	Sequence 180, App
45	44.8	2.4	1071	4	US-09-095-855-180	Sequence 180, App

ALIGNMENTS

RESULT 1
US-08-153-848-39/c
: Sequence 39, Application US/0815384B
: Patent No. 5759804

: GENERAL INFORMATION:
: APPLICANT: Godiska, Ronald
: APPLICANT: Gray, Patrick W.
: APPLICANT: Schweikart, Vicki L.
: TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
: NUMBER OF SEQUENCES: 64
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
: ADDRESSEE: Bicknell
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/153,848
: FILING DATE:
: PRIOR APPLICATION DATA:
: CLASSIFICATION: 514
: APPLICATION NUMBER: US 07/977,452
: FILING DATE: 17-NOV-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5759804and, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 31794
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 39:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1872 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 202..1341
US-08-153-848-39

RESULT 2

US-09-299-843A-39/c
Sequence 39, Application US/09299843A
Patent No. 6107475

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Query Match    3.0%;  Score 56.4;  DB 1;  Length 1872;
Best Local Similarity   52.6%;   Pred. No. 8.2e-05;
Matches  123;  Conservative   0;  Mismatches  111;  Indels   0;  Gaps   0;

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Qy  1457  CAGGAGCGCGGTTGATGAGGACCGAGCTCAGGTTAGAAAAACGTCTCCGAGAAGGGAGGAGGAT 1516
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Db  1125  GAGGAAGGGGTTGAGGCAGCAGTGTTGACGTAGCTGCAGTGGGAGAGATGTT 1066

Qy  1517  CATGTACGCCCCGGAAGTAGGACCTCGTCCAGTCGTTGCTTGGGTTTGGGCCGAGCCCATGAT 1576
          ||| || ||  || || | |||  ||| || || |||  ||||  ||||| |||||
Db  1065  CATGAGGAAGAGGTCAAAGTCACAGGGCCCAGTGCAGCACGGCCTGCCAGGTACACGGT 1006

Qy  1577  CCTCCGAATCTTGGTTGGGCATCCACGATACGGGCCAATGTCACAACAATCAGCCC 1630
          | ||| ||| ||| |||||| ||||| | | ||||| ||| ||||| || |||||
Db  1005  CTTCACCAGGTGGTAGGGCATCCACGCACAGGGCGAAAGGTCACCACCAGCACCAC 952
```

GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
  ADDRESSEE: Borun
  STREET: 6300 Sears Tower, 233 South Wacker Drive
  CITY: Chicago
  STATE: Illinois
  COUNTRY: USA
  ZIP: 60606
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/299,843A
  FILING DATE:
  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 09/088,337
  FILING DATE: 01-Jun-1998
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/153,848
  FILING DATE: 17-Nov-1993
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/977,452
  FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
  NAME: Jill E. Uhl
  REGISTRATION NUMBER: 43,213
  REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (312) 474-6300
  TELEFAX: (312) 474-0448
  TELEX:
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
  LENGTH: 1872 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:

NAME/KEY: CDS
LOCATION: 202..1341
US-09-299-843A-39

RESULT 3

US-09-088-337B-39/c
Sequence 39, Application US/09088337B
Patent No. 6348574

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Query Match    3.0%;  Score 56.4;  DB 3;  Length 1872;
Best Local Similarity   52.6%;   Pred. No. 8.2e-05;
Matches  123;  Conservative   0;  Mismatches  111;  Indels   0;  Gaps   0;

Qy  1397  CAGGCGGCGAGCACGACCACTGCACGAACACCCCGGAAACTGCTCGAGGACACCGTGTA 1456
          | ||| ||| ||||  ||||
Db  1185  CTGGCCACAGCAGCACGCATTGGGAGGTGCAGGGCCTGGGCGGGGGTCGAAAAGGCATA 1126

Qy  1457  CAGGAGCGCGGTTGATGAGGACCGAGCTCAGGTTAGAAAAACGTCTCCGAGAAGGGAGGAGGAT 1516
          || ||| || || || || || ||| |||||| |||||| |||| |||||||||||||
Db  1125  GAGGAAGGGGTTGAGGCAGCAGTGTTGACGTAGCTGCAGTGGGAGAGATGTT 1066

Qy  1517  CATGTACGCCCCGGAAGTAGGACCTCGTCCAGTCGTTGCTTGGGTTTGGGCCGAGCCCATGAT 1576
          ||| || ||  || || | |||  ||| || || |||  ||||  ||||| |||||
Db  1065  CATGAGGAAGAGGTCAAAGTCACAGGGCCCAGTGCAGCACGGCCTGCCAGGTACACGGT 1006

Qy  1577  CCTCCGAATCTTGGTTGGGCATCCACGATACGGGCCAATGTCACAACAATCAGCCC 1630
          | ||| ||| ||| |||||| ||||| | | ||||| ||| ||||| || |||||
Db  1005  CTTCACCAGGTGGTAGGGCATCCACGCACAGGGCGAAAGGTCACCACCAGCACCAC 952
```

GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
       Gray, Patrick W.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
       Schweikart, Vicki L.
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
       Borun
  STREET: 6300 Sears Tower, 233 South Wacker Drive
  CITY: Chicago
  STATE: Illinois
  COUNTRY: USA
  ZIP: 60606
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/088,337B
  FILING DATE: 01-Jun-1998
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/153,848
  FILING DATE: 17-Nov-1993
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/977,452
  FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
  NAME: No. 6348574and, Greta E.
  REGISTRATION NUMBER: 35,302
  REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (312) 474-6300
  TELEFAX: (312) 474-0448
  TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
  LENGTH: 1872 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:

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RESULT 4
PCT-US93-11153-39/c
Sequence 39, Application PC/TUS9311153
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
             Bicknell
  STREET: 6300 Sears Tower, 233 South Wacker Drive
  CITY: Chicago
  STATE: Illinois
  COUNTRY: USA
  ZIP: 60606
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: PCT/US93/11153
  FILING DATE:
  CLASSIFICATION:
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/977,452
  FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
  NAME: Noland, Greta E.
  REGISTRATION NUMBER: 35,302
  REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (312) 474-6300
  TELEFAX: (312) 474-0448
  TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 39:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 1872 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: DNA (genomic)
  FEATURE:
    NAME/KEY: CDS
    LOCATION: 202..1341
```

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US-09-088-337B-39
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
  LOCATION: 202..1341
  NAME/KEY: CDS

Query Match     3.0%;   Score 56.4;  DB 4;  Length 1872;
Best Local Similarity  52.6%;   Pred. No. 8.2e-05;
Matches 123;  Conservative  0;  Mismatches 111;  Indels  0;  Gaps  0;

Qy  1397  CAGGCGGGCACCACCACCTTCCACGAACACCGCCGAAACTGCTGGGGACACCTGTA 1456
Db  1185  CTGGCCACCAGCAGCCATGAGGTCAGGGCCTGCAGGGGGGTCGAAAAAGGCATA 1126
Qy  1457  CAGGAGCGCGGTTGATGACCGAGCTGAGGTAGAAAAACGTCTCCGAGAAGGGAGGAGGAGGAT 1516
Db  1125  GAGGAAGGGGGTTGAGGCAGCTGTTGACGTAGCTCAGGTGCAGTAGGGGAAGAGATGTT 1066
Qy  1517  CATGTACGCCCGGAAGTAGGACCTCGTCGTTCAGTCGTCGTGCTTGGGTTTGGCCGCCATGAT 1576
Db  1065  CATGAGGAAGAGGTCAAAGTCACAGGGCCAGTGCCACGGCCATGTACAGCGT 1006
Qy  1577  CCTCCGAATCTGGTTGGGCATCCAGCATACGGACACAGGGCAAAAGGTCACCACCAGCACCAC 1630
Db  1005  CTTCACCAGGTGGTGAGGGCATCCAGCACACAGGGCCAATGTCACACAACAATCAGCCC 952
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PCT-US93-11153-39

Query Match     3.0%;   Score 56.4;  DB 5;  Length 1872;
Best Local Similarity  52.6%;   Pred. No. 8.2e-05;
Matches 123;  Conservative  0;  Mismatches 111;  Indels  0;  Gaps  0;

Qy  1397  CAGGCGGGCACCACCACCTTCCACGAACACCGCCGAAACTGCTGGGGACACCTGTA 1456
Db  1185  CTGGCCACCAGCAGCCATGAGGTCAGGGCCTGCAGGGGGGTCGAAAAAGGCATA 1126
Qy  1457  CAGGAGCGCGGTTGATGACCGAGCTGAGGTAGAAAAACGTCTCCGAGAAGGGAGGAGGAGGAT 1516
Db  1125  GAGGAAGGGGGTTGAGGCAGCTGTTGACGTAGCTCAGGTGCAGTAGGGGAAGAGATGTT 1066
Qy  1517  CATGTACGCCCGGAAGTAGGACCTCGTCGTTCAGTCGTCGTGCTTGGGTTTGGCCGCCATGAT 1576
Db  1065  CATGAGGAAGAGGTCAAAGTCACAGGGCCAGTGCCACGGCCATGTACAGCGT 1006
Qy  1577  CCTCCGAATCTGGTTGGGCATCCAGCATACGGACACAGGGCAAAAGGTCACCACCAGCACCAC 1630
Db  1005  CTTCACCAGGTGGTGAGGGCATCCAGCACACAGGGCCAAAAGGTCACCACCAGCACCAC 952
```

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RESULT 5
US-09-135-994-1
Sequence 1, Application US/09135994A
Patent No. 6280938
GENERAL INFORMATION:
  APPLICANT: Ranum et al.
  TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
  FILE REFERENCE: University of Minnesota
  CURRENT APPLICATION NUMBER: US/09/135,994A
  CURRENT FILING DATE: 1998-08-18
  EARLIER APPLICATION NUMBER: 60/056,170
  EARLIER FILING DATE: 1997-08-19
  NUMBER OF SEQ ID NOS: 14
  SOFTWARE: PatentIn Ver. 2.0
  SEQ ID NO 1
    LENGTH: 477
    TYPE: DNA
    ORGANISM: Homo sapiens
US-09-135-994-1

Query Match     2.9%;   Score 55.6;  DB 4;  Length 477;
Best Local Similarity  56.2%;   Pred. No. 6.9e-05;
Matches 126;  Conservative  0;  Mismatches 94;  Indels  4;  Gaps  1;

Qy   22  GCTCGGCCCCGGGGAGCGCGGAGCGGAGGAGCAGGAGGACCCAGCGCGGGAGGAGCCCGAGCGCGG 81
Db   84  GCGCCCGCGCGGCGGGCGCGGCGGGCGGAGCAGCGG 143
Qy   82  GCGATGCAGGGTCCGGGAGCGCGGCCACCTGGCGGCCTCCTCTPAAGCTACACCGTGCGTCTCCGC 141
Db  144  GCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC----AGCAGCAGCAGCAGCAGCAGCA 199
Qy  142  GGCAGCAGCGCGGCGCCCCAGCAGCCTCGGCAGCCACAGCCGCTGCAGCCGGCAGCCTC 201
Db  200  AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 259
Qy  202  CGCTGCTGTGTCCGCCTCCTCTGATGCGGCTTGCCCTCTCCGGGCCCC 245
Db  260  AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCGCCGCGCCTCCGCAGCCC 303
```

```
RESULT 6
US-08-118-200-1/c
Sequence 1, Application US/08118200
Patent No. 6137500
GENERAL INFORMATION:
  APPLICANT: SUTHERLAND, Grant R
  APPLICANT: RICHARDS, Robert I
  APPLICANT: SCHLESSINGER, David
  APPLICANT: NAGARAJA, Ramaiah
```

RESULT 7
US-08-458-745-1/c

APPLICANT: KREMER, Eric J
APPLICANT: YU, Sui
APPLICANT: BAKER, Elizabeth
APPLICANT: MULLEY, John C
APPLICANT: MANDEL, Jean-Louis
APPLICANT: PRITCHARD, Melanie April
APPLICANT: LYNCH, Michael
TITLE OF INVENTION: DNA SEQUENCES RELATED TO ISOLATED
TITLE OF INVENTION: FRAGILE X SYNDROME
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,200
FILING DATE: 09-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/802,650
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,232
FILING DATE: 20-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/638,518
FILING DATE: 04-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/966,517
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 020160-164
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1028 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-118-200-1

Query Match 2.9%; Score 55.4; DB 4; Length 1028;
Best Local Similarity 61.4%; Pred. No. 0.00011;
Matches 89; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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Qy  100 GCGGCACCTGGGCTCCTCTAAGCTAGACCGTTCGTCTCCCGGCGAGCGCGGGGCCC 159
        |  ||| |||| |  |||||||| | |||||||||||||||||||||||||||||||||
Db  485 GTGGCTCCGGGCGCCGCCCGCGCGCGCGCGCGCGGGGCGGCGCGGCGCGCGCGCCGCGCC 426

Qy  160 AGCAGCCTCGGCAGCCACAGCCCGCTGCAGCCTCCGCTGCTGTTCGCCTTCTC 219
        |  ||| |  |||||||||| |||| |||||||||||| || |||| ||| |
Db  425 CGCGCGGCCCCACCGCGCGCGCGCGCGCGGCGCGCGCGCGGCGGCGGCGCCGC 366

Qy  220 TGATGCGCCTTGCCCTCTCCCGGCCC 244
        |||| |||||||||||| |||||||
Db  365 CGCGCGCGCGGCTCGCGCGTCGGGCCC 341
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Sequence 1, Application US/08458745
GENERAL INFORMATION:
Patent No. 6242576
APPLICANT: SUTHERLAND, Grant R
APPLICANT: RICHARDS, Robert I
APPLICANT: SCHLESSINGER, David
APPLICANT: NAGARAJA, Ramaiah
APPLICANT: KREMER, Eric J
APPLICANT: YU, Sui
APPLICANT: BAKER, Elizabeth
APPLICANT: MULLEY, John C
APPLICANT: MANDEL, Jean-Louis
APPLICANT: PRITCHARD, Melanie April
APPLICANT: LYNCH, Michael
TITLE OF INVENTION: DNA SEQUENCES RELATED TO ISOLATED
TITLE OF INVENTION: FRAGILE X SYNDROME
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,745
FILING DATE: 02-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/118,200
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/802,650
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,232
FILING DATE: 20-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/638,518
FILING DATE: 04-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/966,517
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 020160-164
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1028 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-458-745-1

Query Match 2.9%; Score 55.4; DB 4; Length 1028;
Best Local Similarity 61.4%; Pred. No. 0.00011;
Matches 89; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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Qy  100 GCGGCACCTGGGCTCCTCTAAGCTACGACCGTTCGTCTCCCGGCGAGCAGCGCGGGGCCC 159
        |  ||| |||| | |||||||| | ||||||||||||||||||||||||||||||||||
Db  485 GTGGCTCCGGGCGCCGCCCGCGCGCGCGCGCGCGGGGCGGCGCGGCGCGCGCGCCGCGCC 426

Qy  160 AGCAGCCTCGGCAGCCACAGCCCGCTGCAGCCTCCGCTGCTGTTCGCCTTCTC 219
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Db 425 CGCCGCCGCCGCCGCCGCCGCCGCCACCGCCGCCGCGCGCCGCGCCGCGCCGGCGCCGC 366
Qy 220 TGATGCGCTTTGCCCTTCTCCGGCCC 244
Db 365 CGCCGCCGCGCCTCGCCGGTCGGCCC 341

RESULT 8
US-08-457-273B-41
Sequence 41, Application US/0457273B
Patent No. 5849995
GENERAL INFORMATION:
; APPLICANT: Hayden, Michael
; APPLICANT: Lin, Blaoyang
; APPLICANT: Nasir, Jamal
; TITLE OF INVENTION: Mouse Model for Huntington's Disease and
; TITLE OF INVENTION: Related DNA Sequences
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Virginia Bennett
; STREET: PO Box 37428
; CITY: Raleigh
; STATE: No. 5849995th Carolina
; COUNTRY: US
; ZIP: 27627
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,273B
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Virginia C.
; REGISTRATION NUMBER: 37,092
; REFERENCE/DOCKET NUMBER: 3477-85A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-854-1400
; TELEFAX: 919-854-1401
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10348 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-457-273B-41

Query Match   2.7%; Score 50.8; DB 2; Length 10348;
Best Local Similarity   64.4%;   Pred. No. 0.0049;
Matches   76; Conservative   0; Mismatches 42; Indels   0; Gaps   0;

Qy 129 CCGTCGTCTCCCGCGGCACCAGCCGCGGGCGCCCAGCCACCAGCCGCTGCAG 188
Db 439 CCACCGCCGCGCCGCCGCCGCCTCCTCACCTTCCTCAGCGCGCCGCCGCCAGGCACAG 498
Qy 189 CCGGGGCAGCCTCCGCTCGTCGCCTCCTCTGATGCGCTTCCCTTCCCGGCCCCG 246
Db 499 CCGCTGCTGCCTCAGCCGCAGCCGCCGCCCCCGCCGCCCCCGCCGCCACCGGCCCGG 556

RESULT 9
US-08-556-419-13
Sequence 13, Application US/0856419C
Patent No. 6093549
GENERAL INFORMATION:
; APPLICANT: Ross, Christopher
; APPLICANT: Li, Xiao-Jiang
; APPLICANT: Li, Shi-Hua
; APPLICANT: Sharp, Alan
; APPLICANT: Lanahan, Anthony
; APPLICANT: Worley, Paul
; APPLICANT: Snyder, Solomon
; TITLE OF INVENTION: Huntingtin-associated protein
; FILE REFERENCE: 01107.52271
; CURRENT APPLICATION NUMBER: US/08/556,419C
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 10348
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-556-419-13

Query Match   2.7%; Score 50.8; DB 3; Length 10348;
Best Local Similarity   64.4%;   Pred. No. 0.0049;
Matches   76; Conservative   0; Mismatches 42; Indels   0; Gaps   0;

Qy 129 CCGTCGTCTCCCGCGGCACCAGCCGCGGGCGCCCAGCCACCAGCCGCTGCAG 188
Db 439 CCACCGCCGCGCCGCCGCCGCCTCCTCACCTTCCTCAGCGCGCCGCCGCCAGGCACAG 498
Qy 189 CCGGGGCAGCCTCCGCTCGTCGCCTCCTCTGATGCGCTTGCCCTTCCCGGCCCCG 246
Db 499 CCGCTGCTGCCTCAGCCGCAGCCGCCGCCCCCGCCGCCCCCGCCGCCACCGGCCCGG 556

RESULT 10
US-09-041-886-14
Sequence 14, Application US/09041886
Patent No. 6235872
GENERAL INFORMATION:
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Rabizadeh, Sharroz
; TITLE OF INVENTION: Proapoptotic Peptides, Dependence
; TITLE OF INVENTION: Polypeptides and Methods of Use
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,886
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2626
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10348 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 316..9748
US-09-041-886-14

Query Match   2.7%; Score 50.8; DB 4; Length 10348;

Best Local Similarity 64.4%; Pred. No. 0.0049;
Matches 76; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

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Qy  129  CCGTGTCTTCCGCGCGGCAGCAGCGGGGGCCCAGCAGCCTGGCAGCCACCACAGCCGCTGCAG  188
         ||| ||||| ||||| |||||||||||||||  ||||||||||| |||||||| ||||||||||
Db  439  CCACCGCCGCGCGCCGCGCCGCCTTCCTCAGCGTTCCTCAGCGGCCGCGCGCCGCAGGCACAG  498

Qy  189  CCGGGGCAGGCCTTCCGCTGTGTTCGGCCGCGCTTGCCCTTCTCCCGGCCCCG  246
         ||| ||||||||||||||||||||||||||||||| || |||||||||||| |
Db  499  CCGCTGCTGCCTCAGCCGCAGCCCGCCCCGCCCCGCCCCCACCCGGCCCGG  556
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RESULT 11
US-08-246-982A-5
Sequence 5, Application US/0824/6982A
Patent No. 5686288
GENERAL INFORMATION:
  APPLICANT: MacDonald, Marcy E.
  APPLICANT: Ambrose, Christine M.
  APPLICANT: Duyao, Mabel P.
  APPLICANT: Gusella, James F.
  TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
  NUMBER OF SEQUENCES: 25
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Sterne, Kessler, Goldstein & Fox
    STREET: 1100 New York Avenue
    CITY: Washington
    STATE: D.C.
    COUNTRY: U.S.A.
    ZIP: 20005
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/246,982A
    FILING DATE: May 20, 1994
    CLASSIFICATION: 435
  ATTORNEY/AGENT INFORMATION:
    NAME: Goldstein, Jorge, A.
    REGISTRATION NUMBER: 29,021
    REFERENCE/DOCKET NUMBER: 0609.3880002
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (202) 371-2600
    TELEFAX: (202) 371-2540
  INFORMATION FOR SEQ ID NO: 5:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 10366 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  FEATURE:
    NAME/KEY: CDS
    LOCATION: 316..9748

US-08-246-982A-5

Query Match 2.7%; Score 50.8; DB 1; Length 10366;
Best Local Similarity 64.4%; Pred. No. 0.0049;
Matches 76; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

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Qy  129  CCGTGTCTTCCGCGCGGCAGCAGCGGGGGCCCAGCCACCAGCCGCTGCAG  188
         ||| ||||| ||||| ||||||||||||||||  |||||||| ||||||||||
Db  439  CCACCGCCGCGCGCCGCGCCGCCTTCCTCAGCGTTCCTCAGCGGCCGCGCGCCGCAGGCACAG  498

Qy  189  CCGGGGCAGGCCTTCCGCTGTGTTCGGCCGCGCTTGCCCTTCTCCCGGCCCCG  246
         ||| ||||||||||||||||||||||||||||||| || |||||||||||| |
Db  499  CCGCTGCTGCCTCAGCCGCAGCCCGCCCCGCCCCGCCCCCACCCGGCCCGG  556
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RESULT 12
US-08-453-265-5
Sequence 5, Application US/08453265

Patent No. 5693757
GENERAL INFORMATION:
  APPLICANT: MacDonald, Marcy E.
  APPLICANT: Ambrose, Christine M.
  APPLICANT: Duyao, Mabel P.
  APPLICANT: Gusella, James F.
  TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
  NUMBER OF SEQUENCES: 25
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Sterne, Kessler, Goldstein & Fox
    STREET: 1100 New York Avenue
    CITY: Washington
    STATE: D.C.
    COUNTRY: U.S.A.
    ZIP: 20005
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/453,265
    FILING DATE: 30-MAY-1995
    CLASSIFICATION: 514
  ATTORNEY/AGENT INFORMATION:
    NAME: Ludwig, Steven R.
    REGISTRATION NUMBER: 36,203
    REFERENCE/DOCKET NUMBER: 0609.3880003
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (202) 371-2600
    TELEFAX: (202) 371-2540
  INFORMATION FOR SEQ ID NO: 5:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 10366 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  FEATURE:
    NAME/KEY: CDS
    LOCATION: 316..9748

US-08-453-265-5

Query Match 2.7%; Score 50.8; DB 1; Length 10366;
Best Local Similarity 64.4%; Pred. No. 0.0049;
Matches 76; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

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Qy  129  CCGTGTCTTCCGCGCGGCAGCAGCGGGGGCCCAGCCACCAGCCGCTGCAG  188
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Db  439  CCACCGCCGCGCGCCGCGCCGCCTTCCTCAGCGTTCCTCAGCGGCCGCGCGCCGCAGGCACAG  498

Qy  189  CCGGGGCAGGCCTTCCGCTGTGTTCGGCCGCGCTTGCCCTTCTCCCGGCCCCG  246
         ||| ||||||||||||||||||||||||||||||| || |||||||||||| |
Db  499  CCGCTGCTGCCTCAGCCGCAGCCCGCCCCGCCCCGCCCCCACCCGGCCCGG  556
```

RESULT 13
US-08-232-463-14
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
  APPLICANT: DORNER, F.
  APPLICANT: SCHEIFLINGER, F.
  APPLICANT: FALKNER, F. G.
  TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
  NUMBER OF SEQUENCES: 52
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Foley & Lardner
    STREET: 1800 Diagonal Road, Suite 500
    CITY: Alexandria
    STATE: VA
    COUNTRY: USA
    ZIP: 22313-0299
  COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE: 26-AUG-1991
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pT2gpt-F1s
US-08-232-463-14

Query Match   2.7%; Score 50.4; DB 1; Length 7218;
Best Local Similarity   2.4%; Pred. No. 0.0052;
Matches   9; Conservative 221; Mismatches 152; Indels   0; Gaps   0;

Qy   449 GGGATCAATGTACCGCAAGTCCTTGTGCATCATCAGCGGCCGTGTCTCATCGGCTCTTGCCGGG 508
          | || | | |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1062 GGCGATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1121

Qy   509 TACCAGTCCTTCTGCTCCCCAGGGAAACTGAACTCAGTTTGCATCAGCTGCTGCAAACACC 568
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Db   1122 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1181

Qy   569 CCTCTTTGTTAACGGGCCAAGGCCCAAGAAAGAGGGAAGTTCTGCCTCGGCCCTCAGGCCA 628
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Db   1182 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1241

Qy   629 GGGCTCCGCACCACCATCCTGTTCCTCAAAATTAGCCCTTCTTCTCGGGCACACTCGTGAAGC 688
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Qy   689 TGAAGGAGATGCCACCCCTCCTGCATTGTTCTTCCAGCCCTCGCCCCCCAACCCCCCACC 748
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Db   1302 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1361

Qy   749 TCCCTGAGTGAGTTTCTTCTGGGTGTGCCTTTTATTCTGGGTAGGGAGGGGAGTCCGTGT 808
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Db   1362 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1421

Qy   809 TCTCTTTTTTGTTCCTGTGCAAAT 830
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Db   1422 YYYYYYYYYYYYGTACCAAAT 1443

; RESULT 14
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.

; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match   2.6%; Score 50.2; DB 4; Length 4403765;
Best Local Similarity   51.1%; Pred. No. 0.12;
Matches 118; Conservative   0; Mismatches 113; Indels   0; Gaps   0;

Qy   25 CGGCCCGGGAGCCGAGCGGGGAGGAGGACAGAGACACCCGCCAGCCCGAGCCCGAGGGGGGCGG 84
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Db 338476 CGGCCCCGCGCGGCGCCCCGGTTGGCCGCCGAAAGCGGCTGGGAATCCGCCGGGACCGGGG 338535

Qy   85 ATGCAAGGCTCCGCGAGGGGCAACCTGCGGCGCTCCTTCTCTAAGCTACGAACCCGTCGTCTCCGGGGC 144
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Db 338536 CCCCGCGGGCCCCCGAACAGCATGCCCGGCGCCCCGCGCCCCGCGCCCCCCGGGGTCC 338595

Qy   145 AGCAGCGCCGGGGCCCCCAGCAGCGTTCGGCAGCCACAGCGCGTGCAGCCGCGGCAGCCTTCCGG 204
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Db 338596 CCGTGCTTGGCCCCTTCCCCCGCGCGCCGGGCCCGGCGCGGCCGGGGGACTCCGG 338655

Qy   205 TGCTGTGTCGCCTCCTTCGATGGGCTTGCCCTTCCCGGCGGCGGCGGCGGCGGGCGCCGGGCGCGG 255
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Db 338656 CGCCGTTGCCGCCGCCGCCGCCCGCGCCGTTGACGCCGCGGGGATCCTCCGG 338706

; RESULT 15
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.

; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match   2.6%; Score 50.2; DB 4; Length 4411529;
Best Local Similarity   51.1%; Pred. No. 0.12;
Matches 118; Conservative   0; Mismatches 113; Indels   0; Gaps   0;

Qy   25 CGGCCCGGGAGACGCGAGCGGGGAGGAGGACAGAGACACCCGCCAGCCCGAGCCCGAGGGGCG 84
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Db 338420 CGGCCCGCGCGGCGCCGGCGCCGGTGGCGCCGGAAAGCGGCTGGGAATCCGCCGGGACCGGGA 338479

Qy   85 ATGCAAGGCTCCGCGAGGGGCGACACCTGCGGCGTCCTTCTTAAGCTACGAACCGTTCTCCGGGGC 144
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Db 338480 CCCCGCGGCGCCCCGAACAGCAATGCCCGGCGCCCCGCGCCCCGAAACAGCAGCATGCCCGGTCC 338539

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Qy     145 AGCAGCGCGGGGCCCCAGCAGCCTCGGCAGCCACAGCCGCTGCAGCCGGGGCAGCCTCCGC 204
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Qy     205 TGCTGTCCGCCTCCTTCTGATGCGCTTGCCCTTCTCCGGCCCCGGGACTCCGG 255
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Db  338600 CGCCGTTGCCGCCCGGCCCCGCCCGCGCCCGTTGACGGCGGGCGCGCCCGGATCCTCCGG 338650
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Search completed: November 7, 2002, 16:56:44
Job time : 3539.08 secs

OM nucleic - nucleic search, using sw model

GenCore version 5.1.3
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Run on: November 7, 2002, 13:45:13 ; Search time 82.4417 Seconds
(without alignments)
8163.686 Million cell updates/sec

Title: 1897
Perfect score: 1897
Sequence: US-09-970-966-214
Sequence: 1 gccaactccggaggctctgg.........aaaaaaaaaaaaaaaaaaaa 1897

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 320260 seqs, 177392727 residues

Total number of hits satisfying chosen parameters: 640520

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

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Published_Applications_NA:*
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12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
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SUMMARIES

Result NO.	Score	% Match	Query Length	DB	ID	Description
c 1	1896.2	100.0	1897	10	US-09-825-294-214	Sequence 214, App
c 2	1606.2	84.7	1619	10	US-09-825-294-205	Sequence 205, App
c 3	1606.2	84.7	1619	10	US-09-825-294-211	Sequence 211, App
c 4	624	32.9	625	10	US-09-825-294-210	Sequence 210, App
c 5	624	32.9	625	10	US-09-867-701-10876	Sequence 10876, A
c 6	566.4	29.9	1010	10	US-09-825-294-212	Sequence 212, App
c 7	508.6	26.8	1362	10	US-09-825-294-208	Sequence 208, App
c 8	476.8	25.1	480	10	US-09-825-294-213	Sequence 213, App
c 9	433.2	22.8	558	10	US-09-867-701-2375	Sequence 2375, Ap
c 10	396.4	20.9	409	10	US-09-867-701-4240	Sequence 4240, Ap
c 11	378.6	20.0	430	10	US-09-867-701-4251	Sequence 4251, Ap
c 12	368.8	19.4	396	10	US-09-825-294-9	Sequence 9, Appl
c 13	365.4	19.3	369	10	US-09-825-294-199	Sequence 199, App
c 14	362	19.1	373	10	US-09-867-701-1516	Sequence 1516, Ap
c 15	354	18.7	390	10	US-09-867-701-1532	Sequence 1532, Ap
c 16	341.8	18.0	381	10	US-09-867-701-7826	Sequence 7826, Ap
c 17	310.2	16.4	349	10	US-09-867-701-2409	Sequence 2409, Ap
c 18	171.2	9.0	201	10	US-09-867-701-8894	Sequence 8894, Ap
c 19	56.4	3.0	1464	10	US-09-149-045-1	Sequence 1, Appl
c 20	50.2	2.6	2038	10	US-09-880-107-2102	Sequence 2102, Ap
c 21	49.4	2.6	1233	10	US-09-749-728B-2	Sequence 2, Appl
c 22	47.8	2.5	2036	10	US-09-866-582-17	Sequence 17, Appl
c 23	47.6	2.5	592	12	US-10-042-417-31	Sequence 31, Appl
c 24	47.6	2.5	2561	12	US-10-023-529-48	Sequence 48, Appl
c 25	47.6	2.5	2561	12	US-10-023-523-48	Sequence 48, Appl
c 26	47.2	2.5	1791	10	US-09-416-384A-6	Sequence 6, Appl
c 27	47.2	2.5	2625	10	US-09-893-238-18	Sequence 18, Appl
c 28	47.2	2.5	4072	10	US-09-893-238-16	Sequence 16, Appl
c 29	47.2	2.5	4051	10	US-09-893-238-14	Sequence 14, Appl
c 30	45.6	2.4	1051	10	US-09-893-238-10	Sequence 10, Appl
c 31	45.6	2.4	2419	10	US-09-893-238-8	Sequence 8, Appl
c 32	45.6	2.4	8827	10	US-09-893-238-1	Sequence 1, Appl
c 33	45.2	2.4	1614	12	US-10-023-529-45	Sequence 45, Appl
c 34	45.2	2.4	1614	12	US-10-023-523-45	Sequence 45, Appl
c 35	45.2	2.4	12425	12	US-10-023-529-50	Sequence 50, Appl
c 36	45.2	2.4	12425	12	US-10-023-523-50	Sequence 50, Appl
c 37	45	2.4	41936	10	US-09-967-768A-116	Sequence 116, App
c 38	44.6	2.4	593	9	US-09-783-252-20	Sequence 20, Appl
c 39	44.6	2.4	1203	9	US-09-945-182-29	Sequence 29, Appl
c 40	44.6	2.4	4563	12	US-10-052-586-311	Sequence 311, App
c 41	44.4	2.3	2462	9	US-09-922-364A-48	Sequence 48, Appl
c 42	43.8	2.3	601	10	US-10-078-929-29	Sequence 29, Appl
c 43	43.8	2.3	894	10	US-09-815-242-4029	Sequence 4029, Ap
c 44	43.6	2.3	6483	10	US-09-880-107-3699	Sequence 3699, Ap
c 45	43.4	2.3	1794	10	US-09-793-306-145	Sequence 145, App

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-09-825-294-214

; Sequence 214, Application US20020044991A1
; Patent No. US20020044991A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 214
; LENGTH: 1897
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1897)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-214

Query Match   100.0%; Score 1896.2; DB 10; Length 1897;
Best Local Similarity   100.0%;
Matches 1897; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GCCAACTCCGGAGGCTCTGGTTGCTCGGCCCCGGAGGCGCGAGCGGGAGCAGAGAGAACCG 60
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Qy   61 CAGCGGGGAGCGCGAGCGCGGCGGATGCAGGCTTCCGGCGACCTTGCGGCTCCTCTA 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CAGCGGGGAGCGCGAGCGCGGCGGATGCAGGCTTCCGGCGACCTTGCGGCTCCTCTA 120

Qy   121 AGCTACGACCGTTCGTCTCCCGCGGCACCAGCGCGGGCCCCACCAGCTCGGCAGCCACAGC 180
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Db   121 AGCTACGACCGTTCGTCTCCCGCGGCACCAGCGCGGGCCCCACCAGCTCGGCAGCCACAGC 180

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Qy    181 CGCTGCAGCCGGGGCGGGGCAGCCTCCGCTGCTGTGCTGCCTTGATCGCTTCCTCTGATCGCTTGCCCTTCTCCCG 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CGCTGCAGCCGGGGCGGGGCAGCCTCCGCTGCTGTGCTGCCTTGATCGCTTCCTCTGATCGCTTGCCCTTCTCCCG 240

Qy    241 GCCCCGGGGGACTCCGGGAGAATGTGGGTCCTAGGCATCGGGCAACTTTTTTGCGGATTGTT 300
          |||||||||||||||||||||||||||||||||||||||||    ||||||||||||||||||
Db    241 GCCCCGGGGGACTCCGGGAGAATGTGGGTCCTAGGCATCGGGC||||CTTTTTTGCGGATTGTT 300

Qy    301 CTTGCTTCCAGGCCTTTGGCGCTCGCAAAATCCAGTGCTACCAGTGTGAGAGAATTCCAGCTGAA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTTGCTTCCAGGCCTTTGGCGCTCGCAAAATCCAGTGCTACCAGTGTGAGAGAATTCCAGCTGAA 360

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Db    361 CAACGACTGCTCCTCCCCCGAGTTCATTGTGAATTGCACGGAGACAATGTG 420

Qy    421 TCAGAAAAGAAAGTGATGGAGCAAAAGTGCCGGGATCATGTACCGCAAGTTCCTTGTGTGCATCATC 480
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Db    421 TCAGAAAAGAAAGTGATGGAGCAAAAGTGCCGGGATCATGTACCGCAAGTTCCTTGTGTGCATCATC 480

Qy    481 ACCGGGCCTGTGTCTCATCGGCCTGCCGGGTACCAGTCCTTGTCTCCCAGGGAAAACTGAA 540
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Db    481 ACCGGGCCTGTGTCTCATCGGCCTGCCGGGTACCAGTCCTTGTCTCCCAGGGAAAACTGAA 540

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Db    541 CTCAGTTTTGCATCAGCGTGCAACACACCCCTCTTTGTAACGGGCCAAGGCCCAAGAAAAG 600

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Db    601 GGGAAGTTCTGCCTCGGCCTCAGGCGCCACCACCCCTCTTTGTAACGGCCAAGGCCCAAAATT 660

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Db    661 AGCCCTCTTCTCGGCACACTGCTTGAAGCTGAAGGATGCCACCACCCCTCCTGCATTGTTC 720

Qy    721 TTCCAGCCCTCGCCCCCAACCCCCCAACCCCTCCCTGAGTGAGTTTCTTCTGTGTCCTTTT 780
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Db    721 TTCCAGCCCTCGCCCCCAACCCCCCAACCCCTCCCTGAGTGAGTTTCTTCTGTGTCCTTTT 780

Qy    781 ATTCTGGGTAGGGAGCGGGAGTCCGTGTTCTCTTTTTGTTCCTGGTGCAAATAATGAAAGAGG 840
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Db    781 ATTCTGGGTAGGGAGCGGGAGTCCGTGTTCTCTTTTTGTTCCTGGTGCAAATAATGAAAGAG 840

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Db    841 CTCGGTAAAGCATTCTGAATAAATTCAGCYTGACTGAATTTTCAGTATGTACTTGAAGGA 900

Qy    901 AGGAGGTGGAGTGAAAGTTCACCCCCATGTCTCGTGTAACGGAGTCAAGGCCAGGCTGGC 960
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Db    901 AGGAGGTGGAGTGAAAGTTCACCCCCATGTCTCGTGTAACGGAGTCAAGGCCAGGCTGGC 960

Qy    961 AGAGTCWGTCCTTAGAAGTCACTCGAGGTGGGCANTCTGCCTTTTGTAAAGCCTCCAGTGTC 1020
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Db    961 AGAGTCWGTCCTTAGAAGTCACTCGAGGTGGGCANTCTGCCTTTTGTAAAGCCTCCAGTGTC 1020

Qy   1021 CATTCCATCCCTGATGGGGCATAGTTGACTGCAGAGTGACGTTTTCTTAG 1080
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Qy   1081 GGCTGGAGGGCCAGTTCCCACTCAAGGGTCCCTTCGCTTGACATTCAAACTTCATGCTCCT 1140
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Db   1081 GGCTGGAGGGCCAGTTCCCACTCAAGGGTCCCTTCGCTTGACATTCAAACTTCATGCTCCT 1140

Qy   1141 GAAAACCATTCTCTGCACAGAATTGGCTGGTTTCGCCCTGAGTTGGGCTCTAGTTGACT 1200
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Qy   1201 CGAGACTCAATGACTGGGACTTAGACTGGGGTTCGCCCTGCTCTGAAAAGTTGCTTAAGA 1260
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Qy   1321 GCACAAAGCGGGGCGTGTCGGTTGGTGGCGTAGTGCTGCCGCAGGCGCTTCTCGTTGGT 1380
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Db   1321 GCACAAAGCGGGGCGTGTCGGTTGGTGGCGTAGTGCTGCCGCAGGCGCTTCTCGTTGGT 1380

Qy   1381 TGGCCGTGCCTGCAGCGACAGGGCGCACGACACCACCGCACCACCGCGCCGAAACTGCT 1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TGGCCGTGCCTGCAGCGACAGGGCGCACGACACCACCGCACCACCGCGCCGAAACTGCT 1440

Qy   1441 GCGAGGACACCGTGTACAGGAGGAGGCGGTTGATGACCGAGCTGAGGTGAGAAAACGTCTCCG 1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GCGAGGACACCGTGTACAGGAGGAGGCGGTTGATGACCGAGCTGAGGTGAGAAAACGTCTCCG 1500

Qy   1501 AGAAGGGGAGGAGGATCATGTACGGCCCGGAAGTAGGACCTGTTCCAGTGTCGTGGGGTT 1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGAAGGGGAGGAGGATCATGTACGGCCCGGAAGTAGGACCTGTTCCAGTGTCGTGGGGTT 1560

Qy   1561 TGGCCCCAGCCATGATCCTTCCGAATCTCAGCATCACCATACGGCCAATGTCACAA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TGGCCCCAGCCATGATCCTTCCGAATCTCAGCATCACCATACGGCCAATGTCACAA 1620

Qy   1621 CAATCAGCCCTGGGCAGACACGAGCAGGAGGAGGAGGAGGAGAAAAACACAGCAT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CAATCAGCCCTGGGCAGACACGAGCAGGAGGAGGAGGAGGAGAAAAACACAGCAT 1680

Qy   1681 GAGACACAGTAAAATGAAATAAAAACCATAAAAATATATTTTAGCCCCTTGTTCTTACTG 1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GAGAACACAGTAAATGAAATAAAAACCATAAAAATATATTTTAGCCCCTTGTTCTTACTG 1740

Qy   1741 GCCAGAAAATGGTACCCAATTTTTCACTGTTGTCGACTTTGACACGTTCTTTTTGCCAAGCAA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCCAGAAAATGGTACCCAATTTTTCACTGTTGTCGACTTTGACACGTTCTTTTTGCCAAGCAA 1800

Qy   1801 GAGAGAAATTTAACACTGTTTTCAAAACCCGGGGGAGTTGGGCTGTGTTGTTAAAGAAAGACCATTA 1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GAGAGAAATTTAACACTGTTTTCAAAACCCGGGGGAGTTGGGCTGTGTTGTTAAAGAAAGACCATTA 1860

Qy   1861 AATGCTTTAGACAGTGTAAAAAAAAAAAAAAAAAA 1897
          |||||||||||||||||||||||||||||||||||
Db   1861 AATGCTTTAGACAGTGTAAAAAAAAAAAAAAAAAA 1897
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RESULT 2
US-09-825-294-205
; Sequence 205, Application US/09825294
; Patent No. US20020004491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 205
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-825-294-205

  Query Match   84.7%; Score 1606.2; DB 10; Length 1619;
  Best Local Similarity   99.8%;
  Matches 1616; Conservative   2; Mismatches   0; Indels   1; Gaps   1;

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Qy    280 GGCAACTTTTTGCGGATTGTTCTTGCTTCCAGGCCTTTGGCGCTCGCAAAATCCAGTGCTACCA 339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGCAACTTTTTGCGGATTGTTCTTGCTTCCAGGCCTTTGGCGCTCGCAAAATCCAGTGCTACCA 60
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Qy    340 GTGTGVAGAATTCCAGCTGAACAACGACTGCTCCTCCCCCGAGTTCATTGTGAATTGCAC 399
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GTGTGAAGAATTCCAGCTGAACAACGACTGCTCCTCCCCGAGTTCATTGTGAATTGCAC 120

Qy    400 GGTGAACGTTCAAGACATGTCAGAAAGAAGTGATGAGGACAGATCATCATGTA 459
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGTGAACGTTCAAGACATGTCAGAAAGAAGTGATGAGGACAGATCATCATGTA 180

Qy    460 CCCCAAGTCCTGTGTGCATCATCAGGGGGGTACCAGTCCTT 519
          ||||||||||||||||||||||||||||||||||||||||||
Db    181 CCCGCAAGTCCTGTGTCATCATCAGGGCCTGTCTCGCGGGTACCAGTCCTT 240

Qy    520 CTGCTCCCCAGGGAAACTGAACTCAGTTTGCATCAGTCGT 579
          |||||||||||||||||||||||||||||||||||||||||
Db    241 CTGCTCCCCAGGGAAACTGAACTCAGTTTGCATCAGTCGT 300

Qy    580 CGGGCCAAGGCCCAAGAAAGGGGAAGTTCTGCCTCAGGCTCCGCAC 639
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGGCCAAGGCCCAAGAAAGGGGAAGTTCTGCCTCAGGCTCCGCAC 360

Qy    640 CACCCATCCTGTTCCTCAAATTAGCCCTTCTTCTCGGCCACACTGTCTGAAGCTGAAGGAGATG 699
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CACCCATCCTGTTCCTCAAATTAGCCCTTCTTCTCGGCCACACTGTCTGAAGCTGAAGGAGATG 420

Qy    700 CCACCCCTTCCTCGCATTGTTCTTCCAGCCCTCGCCCCCAACCCCCCTGAGTGA 759
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CCACCCCTTCCTCGCATTGTTCTTCCAGCCCTCGCCCCCAACCCCCCTGAGTGA 480

Qy    760 GTTTCTTCTGGGTGTCCTTTTATTCTGGGGTAGGGGGAGGT 819
          |||||||||||||||||||||||||||||||||||||||||
Db    481 GTTTCTTCTGGGTGTCCTTTTATTCTGGGTAGGCGGGAGGT 540

Qy    820 CCTGTGTGCAAAATAATGAAAGAGAGCTCGGTAAAGCAITTCTGAATAAATTCAGCYTGACTGGAAT 879
          ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Db    541 CCTGTGTGCAAATAATGAAAGAGAGCTCGGTAAAGCAITTCTGAATAAATTCAGCGTGACTGAAT 600

Qy    880 TTTCAGTTATGTACTTGAAGGAAGGAGGGTGGAGTGAAAGTTCACCCCCATGTCTGTGTAAC 939
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TTTCAGTTATGTACTTGAAGGAAGGAGGGTGGAGTGAAAGTTCACCCCCATGTCTGTGTAAC 660

Qy    940 CGGAGTCAAGGCCCAGGCGTGGCAGAGTCWGTCCTTAGAAGTCACTGAGGGTGGGCATCTGCC 999
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CGGAGTCAAGGCCAGGCTGGCAGAGTCACTCCTTAGAAGTCACTGAGGTGGGCCATCTGCC 720

Qy   1000 TTTTGTAAAGCCTCCAGTGTCCAICCCGAITGAGGGGGCATAGTTGTTGAGACTGCAGA 1059
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TTTTGTAAAGCCTCCAGTGTCCATTCCATCCCTGATGGGGCATAGTTGTTGAGACTGCAGA 780

Qy   1060 GTGAGAGTGACGTTTTCTTAGGGCTGGAGGGCCAGTTCCCACTCAAAGGCTCCCGCTGCTTG 1119
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GTGAGAGTGACGTTTTCTTAGGGCTGGAGGGCCAGTTCCCACTCAAAGGCTCCCGCTTG 840

Qy   1120 ACATTCAAAACTTCATGTCTCCTGAAAACCATTCTTCTGCACAGAAATTGGCTGGTTTTCGCGC 1179
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ACATTCAAAACTTCATGTCTCCTGAAAAACCATTCTTCTGCACAGAAATTGGCTGGTTTTCGCGC 900

Qy   1180 CTGAGTTGGGCTTCTAGTGACTCGAGACTTAGACTGGGGGCTCGGCCCT 1239
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CTGAGTTGGGCTTCTAGTGACTCAATGACTGGGACTTAGACTGGGGGCTCGGCCT 960

Qy   1240 CGCTCTGAAAAAGTGCTTAAGAAAAATCTTCTCACGTTCTCCTTGCAGAGGACTTGCGGCTACC 1299
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CGCTCTGAAAAAGTGCTTAAGAAAAATCTTCTCAGTTCTCCTTGCAGAGGACTTGGCCATGTA 1020

Qy   1300 ACGCGAGAGAGCAAACGGCGCCTGCTGTCGGTGTGGTGAGTGCCGCATGTA 1359
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ACGCGAAGAGAGCAAACGGCGCCTGCTGTCGGTGTGGTGAGTGCCGCATGTA 1080

Qy   1360 CGCGCAGGCGGCTTCGTGGTTGGTTGGGGTTGGCGGCTGCAGCGCAGCACC-TGC 1418
          |||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   1081 CGCGCAGGCGGCTTCGTGGTTGGTTGGGCGGCTGCAGCGCGACAGCACCTTGC 1140
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Qy   1419 ACGAACACCCGCCGAAACTGCTGCGAGGACACCGTGTACAGCGAGGAGGACCGGAG 1478
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ACGAACACCCGCCGAAACTGCTGCGAGGACACCGTGTACAGGAGGAGGACCGGAG 1200

Qy   1479 CTGAGGTAGAAAAAAGTCTCCGAGAAGGGGAGGGAGGGAGGGAGGATCATGTAGCCGCGGAGTAGGAC 1538
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CTGAGGTAGAAAAAAGTCTCCGAGAAGGGGAGGGAGGGAGGATCATGTACGCGGAGTAGGAC 1260

Qy   1539 CTCGTCCAGTCGTGCTTGGGGTTTGGGCGCCGCAGCCATGATCCTCCGAATCTGGGTTGGGCATC 1598
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Db   1261 CTCGTCCAGTCGTGCTTGGGTTTGGGCGCCGCACCCATGATCCTCCGAAATCTGGTTGGGCATC 1320

Qy   1599 CAGCATTACGGGCCAATGTCACAACCAATCACGCCCTGGGCGAGACACGGAGGAGGAGGAGAC 1658
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Db   1321 CAGCATTACGGGCCAATGTCACAACCAATCACGCCCTGGGCGAGACACGGAGGAGGAGAGAC 1380

Qy   1659 AGAGAAAAGAAAAAACAACAGCAATGAGAACACACAGTGAGAAATGGTGAATAAATAATATTGAG 1718
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 AGAGAAAAGAAAAAACACAGCAATGAGAACACAGTGAGAAATGGTACCAATTTTTCAGTGTTGGACTTGA 1440

Qy   1719 CCCCTTCTGTTCTTGTCTTACTGGCCAGAAAATGGTACCAATTTTTCAGTGTTGGACTTGA 1778
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CCCCTTCTGTTCTTGTCTTACTGGCCAGAAAATGGTACCAATTTTTCAGTGTTGGACTTGA 1500

Qy   1779 CAGCTTCTTTTGCCACAAGCAAGAAGAATTTAACACTGTTTCAAACCCGGGGGGAGTTGG 1838
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CAGCTTCTTTTGCCACAAGCAAGAAGAATTAACACTGTTTCAAACCCGGGGGAGTTGG 1560

Qy   1839 CTGTGTTAAAGAAAAGACCCATTAAATGCTTTAGACAGTGTAAAAAAAAAAAAA 1897
          |||||||||||||||||||||||||||:|||||||||||||||||||||||||
Db   1561 CTGTGTTAAAGAAAAGACCATTAAATGCTTTAGACAGTGTAAAAAAAAAAAAAAAAAA 1619
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Qy    280 GGCAACTTTTTGCGGATTGGTTCTTGCTTCCAGGCTTTGCGCTGCAAATCCAGTGCTACCA 339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGCAACTTTTTGCGGATTGGTTCTTGCTTCCAGGCTTTGCGCTGCAAATCCAGTGCTACCA 60

Qy    340 GTGTGAAGAATTCCAGCTGAACAACGACTGCTCCTCCCCCGAGTTCATTGTGAATTGCAC 399
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GTGTGAAGAATTCCAGCTGAACAACGACTGCTCCTCCCCGAGTTCATTGTGAATTGCAC 120

Qy    400 GGTGAACGTTCAAGACATGTCAGAAAGAAGTGATGAGGACAGATCATCATGTA 459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGTGAACGTTCAAGACATGTCAGAAAGAAGTGATGAGGACAGATCATCATGTA 180

Qy    460 CCCGCAAGTCCTGTGCATCATCAGGGGCCCTGTCTCATCGCCCTGTGCGGGTACCAGTCCTT 519
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db 181 CCGGCAAGTCCTGTGCATCATCAGCGGGCCTTGTCTCATCGCCTCTGCCGGTTACCAGTCCTT 240
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Qy 520 CTGCTCCCCAGGGAAACTGAACTCAGTTTTGCATCAGCTGCTGCAACACCCCTCTTTGTAA 579

Db 241 CTGCTCCCCAGGGAAACTGAACTCAGTTTTTGCATCAGCTGCTGCAACACCCCTCTTTGTAA 300
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Qy 580 CGGGCCAAGGCCCAAGAAAAAGGGGAAGTTCTGCCTTCGGCCGCCTCAGGGCCTCCGCAC 639

Db 301 CGGGCCAAGGCCCAAGAAAAAGGGGAAGTTCTGCCTTCGGCCGCCTCAGGGCCTCCGCAC 360
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Qy 640 CACCAATCCTGTTCCTCAAATTAGCCCTCTTCTCCTCGGCCTGCTTGAAAGCTGAAGGAGATG 699

Db 361 CACCAATCCTGTTCCTCAAATTAGCCCTCTTCTCCTCGGCCTGCTTGAAAGCTGAAGGAGATG 420
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Qy 700 CCACCCCTCCTCGCATTGTTCTTCCAGCCCTGCCTCGCCCCACCCCCACCTCCCTGAGTGA 759

Db 421 CCACCCCTCCTCGCATTGTTCTTCCAGCCCTGCCTCGCCCCACCCCCACCTCCCTGAGTGA 480
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Qy 760 GTTTCTTCTTCTGGGTGTCCTTTTATTCTTTATTCTGGGTTAGGGAGGCGGGGAGGTTGTT 819

Db 481 GTTTCTTCTTCTGGGTGTCCTTTTATTCTTTATTCTGGGTTAGGGAGGCGGGGAGGTTGTT 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 820 CCTGTTGCAAATAATGAAAGAGCTCGGTAAAGCATTCTGAATAAATTCAGCCVTGACTGAAT 879

Db 541 CCTGTTGCAAATAATGAAAGAGCTCGGTAAAGCATTCTGAATAAATTCAGCCTGACTGAAT 600
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Qy 880 TTTCAGTATGTTACTTGAAGGAAGGAGGTTGGAGTGAAAGTTCACCCCCCATGTCTGTGTAAC 939

Db 601 TTTCAGTATGTTACTTGAAGGAAGGAGGTTGGAGTGAAAGTTCACCCCCCATGTCTGTGTAAC 660
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 940 CGGAGTCAAGGCCAAGGCTGGCGAGAGTCWGTCCTTAGAAGTCACTGAGGTGGGGCATCTGCC 999

Db 661 CGGAGTCAAGGCCAAGGCTGGCGAGAGTCAGTCCTTAGAAGTCACTGAGGTGGGGCATCTGCC 720
        ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Qy 1000 TTTTGTAAAGCCTCCAGTGTCCATTCCATCCCTGATTGGGGCATAGTTTTGAGACTGCAGA 1059

Db 721 TTTTGTAAAGCCTCCAGTGTCCATTCCATCCCTGATTGGGGCATAGTTTTGAGACTGCAGA 780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1060 GTGAGAGTGACGTTTTTCTTAGGGCTGGAGGGCCAGTGTCCCACTCAAGGCTCCCTCGCTTG 1119

Db 781 GTGAGAGTGACGTTTTTCTTAGGGCTGGAGGGCCAGTGTCCCACTCAAGGCTCCCTCGCTTG 840
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1120 ACATTCAAAACTTCATGCTCTGAAAAACCATTCTCTGCCAGCAGAAATGGGCTGCGCGC 1179

Db 841 ACATTCAAAACTTCATGCTCTGAAAAACCATTCTCTGCCAGCAGAAATGGGCTGCGCGC 900
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Qy 1180 CTGGAGTTGGGCTCTACTAGACTCGAGACTCAATGACTTAGACTGGGGCTCGGCCT 1239

Db 901 CTGGAGTTGGGCTCTACTAGACTCGAGACTCAATGACTTAGACTGGGGCTCGGCCT 960
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1240 CGCTCTGAAAAGTGCTTAAGAAAAATCTTCTCCAGTTCCTTGCAGAGGACTGGCGCCGGG 1299

Db 961 CGCTCTGAAAAGTGCTTAAGAAAAATCTTCTCCAGTTCCTTGCAGAGGACTGGCGCCGGG 1020
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1300 ACGCGAAGAGCAAACGGGGCTGCACAAAGGCGTCGGTGGTCGGAGTGCGCATGTA 1359

Db 1021 ACGCGAAGAGCAAACGGGGCTGCACAAAGGCGTCGGTGGTCGGAGTGCGCATGTA 1080
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Qy 1360 CGGCGCAGGCGCTTCTCGTGGTTGGCTGCTCCAGCGACAGCCACC-TGC 1418

Db 1081 CGGCGCAGGCGCTTCTCGTGGTTGGCTGCTCCAGCGACAGCCACCTGC 1140
        ||||||||||||||||||||||||||||||||||||||||||||| ||
Qy 1419 ACGAACACCCGCGAAACTGCTGCGAGGAGCACCGTGTACAGGAGGAC 1478

Db 1141 ACGAACACCCGCGAAACTGCTGCGAGGAGCACCGTGTACAGGAGGAC 1200
        |||||||||||||||||||||||||||||||||||||||||||||||
Qy 1479 CTGAGGTAGAAAAACGTCTCCGAGAAGGGGAGGTAGTAGGAC 1538

Db 1201 CTGAGGTAGAAAAACGTCTCCGAGAAGGGGAGGTAGTAGGAC 1260
        ||||||||||||||||||||||||||||||||||||||||||
Qy 1539 CTCGTCCAGTCGTGCTTGGGTTTGGGCGCCGGAAGGGGGGC 1598

Db 1261 CTCGTCCAGTCGTGCTTGGGTTTGGGCGCACCCATGATCCTCCGGAATCCTGGTTGGGCATC 1320

RESULT 4
US-09-825-294-210
; Sequence 210, Application US/09825294
; Patent No. US20020044491A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 210
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(625)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-210

Query Match   32.9%; Score 624; DB 10; Length 625;
Best Local Similarity   99.8%; Pred. No. 7.2e-154;
Matches 624; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1599 CAGCATACGGCGCCAAATGTCACAACAACAATCAGCCCTGGGGACAGACGAGGGAGAGAC 1658
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Db 1321 CAGCATACGGCGCCAAATGTCACAACAACAATCAGCCCTGGGGACAGACGAGGGAGAGAC 1380

Qy 1659 AGAGAAAAAGAAAAACACAGCATGAGAACACAGTAAATGAATGAATAAATAATTATTTAG 1718
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1381 AGAGAAAAAGAAAAACACAGCATGAGAACACAGTAAATGAATGAATAAATAATTATTTAG 1440

Qy 1719 CCCCTCTTCTTTCGTGTCGTGCTTACTGCCCAGGAAAATGGTACCAATTTTCAGTGTTGGGGACTTGA 1778
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1441 CCCCTCTTCTTTCGTGTCGTGCTTACTGCCCAGGAAAATGGTACCAATTTTCAGTGTTGGGGACTTGA 1500

Qy 1779 CAGCTTCTTTTGCCACAAGCAAGAGAGAGAATTTTAACACGTTTTTCAAACCCGGGGAGTTGG 1838
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1501 CAGCTTCTTTTGCCACAAGCAAGAGAGAATTTAACACGTTTTTCAAACCCGGGGAGTTGG 1560

Qy 1839 CTGTGTTAAAGAAAGAAAGACCATTAAAATGCTTTAGACAGTGTAAAAAAAAAAAAAAA 1897
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1561 CTGTGTTAAAGAAAGAAAGACCATTAAAATGCTTTAGACAGTGTAAAAAAAAAAAAAAA 1619

Db 301 CATGATCCTCCGAATCTGGTTGGGCCATCCAGCATACGGCCAATGTCACAACAATCAGCCC 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1631 TGGGCAGACACGAGCGAGGAGGAGGAGGAGAGAAAACACAGCATTGAGAACACAG 1690
        |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db 361 TGGGCAGACACGAGGAGGAGGAGGAGGAGAGAAAAACACAGCATTGAGAACACAG 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1691 TAAATGAATAAAAACCATAAAAATATTTAGCCCCTCTCGTTGCCTGCCAGAAAT 1750
        |||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db 421 TAAATGAATAAAAACCATAAAAATATTTAGCCCCTCTCGTTGCCTACTCGGCCAGAAAT 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1751 GGTACCAATTTTTCAGTGTTGGACTTGACAGCTTCTTTTGCCACAGCAAGCAAGAGAGAATTT 1810
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 GGTACCAATTTTTCAGTGTTGGACTTGACAGCTTCTTTTGCCACAGCAAGCAAGAGAGAATTT 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1811 AACACTGTTTCAAACCCGGGGGAGTTGGCTGTGTTTAAAGAAAAGACCATTAAATGCTTTAG 1870
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 AACACTGTTTCAAACCCGGGGGAGTTGGCTGTGTTTAAAGAAAAGACCATTAAATGCTTTAG 600
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1871 ACAGTGTAAAAAAAAAAAAAAAAAAAA 1895
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Db 601 ACAGTGNAAAAAAAAAAAAAAAAAAAAAAAA 625

RESULT 5
US-09-867-701-10876
; Sequence 10876, Application US/0986770l
; Patent No. US20020132237A1
; GENERAL INFORMATION:
;   APPLICANT: Aglate, Paul A.
;   APPLICANT: Jones, Robert
;   APPLICANT: Harlocker, Susan L.
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;   TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
;   FILE REFERENCE: 210121.497
;   CURRENT APPLICATION NUMBER: US/09/867,701
;   CURRENT FILING DATE: 2001-05-29
;   NUMBER OF SEQ ID NOS: 10912
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10876
;   LENGTH: 625
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 607
;   OTHER INFORMATION: n = A,T,C or G
US-09-867-701-10876

Query Match   32.9%; Score 624; DB 10; Length 625;
Best Local Similarity 99.8%; Pred. No.7.2e-154;
Matches 624; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1271 AGTTCTCCTTGCAGAGACTGCGCGCCGGGACTGCGCGGGGGCGGGAGCGCAAGCGCAAGGGGCGCCTGCGGGGCCTGACACAAGCG 1330
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Db   1 AGTTCTCCTTGCAGAGACTGCGCGCCGGGACTGCGCGGGGGCGGGAGCGCAAGCGCAAGCG 60
Qy 1331 GGCGCTGTCGGTGGTGGAGTGCCCATGTACGGCCCAGGCGCCGCCTTCTCGTTCGTTGGCGTGCTG 1390
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GGCGCTGTCGGTGGTGGAGTGCGCATGTACGGCCCAGGCGCCGCCTTCTCGTTCGTTGGCGTGCTG 120
Qy 1391 CAGCGACAGGGGCGCAGCAGCGACGACCTGCACGAAACGCCCGCGAAACTGCTCGGAGGACAC 1450
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 CAGCGACAGGGGCGCAGCAGCGACGACCTGCACGAAACTGCTCGGAGGACAC 180
Qy 1451 CGTGTACAGGAGGAGCGGCGGGTTGAGTACCGAGGTAGAAAAACGTCTCCGAGAAGGGGAG 1510
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 CGTGTACAGGAGGAGCGGGGTTGATGACCGAGCTGAGGTAGAAAAACGTCTCCGAGAAGGGGAG 240
Qy 1511 GAGGATCATGTACGCCCCGGAAGTAGAGCTCGTGCTCGTTGGGTTTGGCCGGCAGC 1570
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 GAGGATCAGTGTACGCCCGGAAGTAGAGACCTCGTCGTCCAGTCGTGCTTGGGTTTGGCCGGCAGC 300

US-09-825-294-212

RESULT 6
US-09-825-294-212
; Sequence 212, Application US/09825294
; Patent No. US20020044291A1
; GENERAL INFORMATION:
;   APPLICANT: Xu, Jiangchun
;   APPLICANT: Stolk, John A.
;   APPLICANT: Algate, Paul A.
;   APPLICANT: Fling, Steven P.
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
;   TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
;   FILE REFERENCE: 210121.484C5
;   CURRENT APPLICATION NUMBER: US/09/825,294
;   CURRENT FILING DATE: 2001-04-03
;   NUMBER OF SEQ ID NOS: 215
;   SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 212
;   LENGTH: 1010
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-825-294-212

Query Match   29.9%; Score 566.4; DB 10; Length 1010;
Best Local Similarity 94.1%; Pred. No.1.2e-138;
Matches 687; Conservative 0; Mismatches 31; Indels 12; Gaps 9;

Qy   58 CCGCAGCCGCGGGAGCCCGAGCGCGGCGGCGATCGCAGGCGTCCGGCGGCCACCTTGCCGCTCCT 117
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CCGCAGCCGCGGGAGCCCGAGCGCGGCGGCGATCGCAGGCGTCCGGCGGCCACCTTGCCGCTCCT 60
Qy 118 CTAAGCTACGACCGTCGTCTCCGC-GGCACGAGC-GCGGCGCCCAGCAGCCTCGGGCAGCC 175
        |||||||||||||||||||||||| |||||||| ||||||||||||||||||||||||||
Db   61 CTAAGCTACGACCGTCGTCTCCGTGGCACGAGCTGCGGGCGCCCAGCCAGCCTCGGCGCAGCC 120
Qy 176 ACACGCGTGCAGCC-GGGGCGCAGCCTCCGCGCGTCGTGCGCGCTCGATGGCGCTGCCCT 234
        |||||||||||||| |||||||||||||||||||||| || |||||||||||||||||
Db 121 ACAGCCGCTGCAGCCGTGGGCGCAGCCTCCGTCGCGCCTCCTCGAATGCGCGTTGCCCT 180
Qy 235 CTCCC-GGCCCGGGACTCCGGAGAATGTGGGTCCTAGGCATCGCGGCCAACTTTTTTGCG 293
        ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 CTCCCTGGCCCGGGACTCCGGAGAGTTGGGGTCCTAGGCATCGCGGCCAACTTTTTTGCG 240
Qy 294 GATTGTTCTTTGCTTCC-AGCCTTTGCGCTGCTCCAAGTCCAGTGTTGAGACGTTCAA 352
        ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db 241 GATTGTTCTTTGCTTCCAAGGCTTTGCGCTGCTCAAATCCAGTGCTACCAGTGTGACGAAGTTC 300
Qy 353 CAGCTGACAACGACTGCTCTCCCCCAGGTTCAATGTGAATTCCACGCGGTGACGTTCAA 412
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Db  301  CAGCTGAACAACGACTGCTCTCCCCGAGTTCATTGTGAATTGCACGGTGAACGTTCAA  360
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Qy  413  GACATGTGTCAGAAAAGAAGTGAATGGAGGACAAAGTGCCGGGATCAATGTACCGCAAGTCCTGT  472
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  GACATGTGTCAGAAAAGAAGTGATGGAGGACAAAGTGCCGGGATCAATGTACCGCAAGTCCTGT  420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  473  GCATCAATCAGCGCGCCTCGTCTCAATCGCCTCTGCCGGGTACCAGTCCTTCTGCTCCCAGG  532
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  GCATCAATCAGCGCGCCTCGTCTCATCGCCTCTGCCGGGTACCAGTCCTTCTGCTCCCAGG  480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  533  AAACTGAACTCAGTTTGCATCAGCTGCTGTGCACACACCCCTCTTTGTAA-CGGGCCAAGGCC  591
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481  AAACTGAACTCAGTTTGCATCAGCTGCTGTGCACACACCCCTCTTTGTAACCGGGCCAAGGCC  540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  592  CAAGAAAAAGGGGAAGTTCTGCCTCGGCCCTCAGGCCAGGGTCCGCACCACCATCCTTGTT  651
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Db  541  CAAGAAAAAGGGGAAGTTCTGCCTCGGCCCTCAGGCCAGGGTCCGCACCACCATCCTTGTC  600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  652  CCTCAAATTA--GCCCTCTTCTCCGGCACACTGCTGAA---GCTGAAGGAGGATGGCCACCC  706
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Db  601  CCTCAAATTAAGCCCTACTTCTCGGCACACTGCTGGGAAGCTTGAAGGAGGAGGGCACCCA  660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  707  CTCCTGCATTGTTCTTCCAGCCCTTCGCCCCCCCCACCCTCCCTGAGTGAGTTTCTT  766
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Db  661  CTCCTGCATAGTCCATCCAGGCCTTCGCCCCCCACACACCCCA-CTCCCTGAGAGCACGCC  719
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  767  CTGGGGTGTCC  776
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Db  720  CAGGGAGACC  729
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Qy  1124  TCAAACTTCAtGCCTCCTGAAAAACCATTCTCTCCGCAGAGAATTGGCTGGGTTGCGCCTGA  1183
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Db  1362  TCAAACTTCAtGCCTCCTGAAAAACCATTCTCTCCGCAGAGAATTGGCTGGGTTGCGCCTGA  1303
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1184  GTTGGGCTCTAGTGACTCGGAGACTCAATGACTCGGGGCCTCGGGCCTCGCCCTCGCT  1243
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1302  GTTGGGCTCTAGTGACTCAATGACTGGGGACTTAGACTCTGGGGGCCTCGGGCCTCGCCCTCGCT  1243
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1244  CTGAAAAGTGCTTAAGAAAAATCTTCTCAGTTCTCCTTGCAGAGGACTGGGGGACAGC  1303
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1242  CTGAAAAGTGCTTAAGAAAAATCTTCTCAGTTCTCCTTGCAGAGGACTGGGGGACAGC  1183
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1304  GAAGAGCAAACGGGGCGCGTGCACAAAGCGGGGCGTGTTGGTGGAGTCGGCCATTGTACCCG  1363
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1182  GAAGAGCAAACGGGGCGCGCTGCACAAAGCGGGGCGTGTCGGTGGAGTCGGCATGTACCG  1123
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Page right column:

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Qy  1364  CAGGGGCTTCTTCTGTGGGTTGGCTGTCTGCGACGAGCGGGCGGCCGGCAGCACCTGCACGAA  1423
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1122  CAGGGGCTTGCTTCTGTGGTTGGCGTGTCGCCACGGCACGGCGGGGCGGCCGGCAGCACCTGCACGAA  1063
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Qy  1424  CACCCGCGCGAAAACTGCTCGGAGGACACCGTGTACAGGAGGGGGTTGATGACGGAGCTGAG  1483
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1062  CACCCGCGCGAAAACTGCTCGGAGGACACCGTGTACAGGAGGGGGTTGATGACGGAGCTGAG  1003
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Qy  1484  GTAGAAAAAAGCTCTCCGAGAAGGGGAGGGGAGGGGAGGGGCATGTACCGCCCGGAAGTAGGACTTCGT  1543
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Db  1002  GTAGAAAAAAGCTCTCCGAGAAGGGGAGGGGGATCAATGTACCGCCCGGAAGTAGGACTTCGT  943
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Qy  1544  CCAGTCGTGCTTGGGTTTGGGCCGCCAGCCATGAGTCCTCCGGAATCTCCGGATCATCTGGTTGGGCCATCCAGCA  1603
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  942  CCAGTCGTGCTTGGGTTTGGGCCGCCAGCCATGATTCTCCGGAATCTGGTTGGGCCATCCAGCA  883
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Qy  1604  TACGGGCCAATGTCACAACAATCAGCCCTGGGCAGA  1638
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Db  882  TACGGCCAATGTCACAACAATCAGCCTCAGGAGAA  848
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Qy  1  GCCAACTCCGGAGGCTCTGGTTGTCTGGCCGCGGAGCGCGGAGCGGAGAGAGAGACCCG  60
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Db  1  GCCAACTCCGGAGGCTCTGGTTGTCTGGCCGCGGAGCGCGGAGCGGAGAGAGAGACCCG  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  61  CAGGCCGGGAGGCCCGAGCGCGGGCGGCCGATGCAGGCTCCGGACAGCCTGCGGCTCCTCTA  120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61  CAGGCCGGGAGGCCCGAGCGCGGGCGGCCGATGCAGGCTCCGGACAGCCTGCGGCTCCTCTA  120
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Qy  121  AGCTACGACCGTGCTGTCTCCGCCGGAGCAGCAGCCCCAGCCAGCCTCGGCCAGCACAGC  180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  AGCTACGACCGTGCTGTCTCCGCCGGAGCAGCAGCCCCAGCCAGCCTCGGCCAGCACAGC  180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  181  CGCTGCAGCCGCGGGGGCAGCCTCCGCGGCGGCCTTGATGCGGCCTTGCCCTCTCCG  240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  CGCTGCAGCCGCGGGGGCAGCCTCCGCGGCGGCCTTGATGCGGCCTTGCCCTCTCCG  240
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Qy  241  GCCCCGGGGACTCCGGAGAATGTGGGTCTTAGGCACCATCGGCGGCAACTTTTTGCGGATTGTT  300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  GCCCCGGGGACTCCGGAGAATGTGGGTCTTAGGCACCATCGGCGGCAACTTTTTGCGGATTGTT  300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  301  CTTGCTTCCAGGCTTTGGCCTGCAAATCCAGTGTCTACCAGTGTGTAGAGAATTCCACGTGAA  360
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Db  301  CTTGCTTCCAGGCTTTGGCCTGCAAATCCAGTGCTACCAGTGTGTAGAGAATTCCACGTGAA  360
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Qy  361  CAACCAGCTGTCTCCCCCGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTG  420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Fri Nov 8 18:57:09 2002   us-09-970-966-214.std.rnpb   Page 7

Left column

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Db   361  CAACGACTGCTTCCCCCGAGTTCATTGTGAATTCCACGGTGAACGTTCAAGACAATGTG  420
          |||||||||||
Qy   421  TCAGAAAGAAGTGATGGAGCAAAAGTGCCGGGGATCCATGTATACCGCAAGTCCTGTCATCATC  480
Db   421  TGAGAAAGAAGTGATGGAGCAAAAGTGCCGGGGATCATGTACCGCAAGTCCTGTGCATGATC  480
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RESULT 9

US-09-867-701-2375

; Sequence 2375, Application US/09867701
; Patent No. US2002013237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; SOFTWARE: FastSEQ for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 10912
; SEQ ID NO 2375
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(558)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-2375

Query Match   22.8%;   Score 433.2;   DB 10;   Length 558;
Best Local Similarity 95.6%;   Pred. No. 6.3e-104;
Matches 539; Conservative   0; Mismatches   14; Indels 11; Gaps 9;

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Qy  1271  AGTTCTCTTGCAGAGGACTGCGGCCCCGGGGAAGAGCAACGGGCGCCTGCACAAAGCG  1330
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Db     1  AGTTCTCCTTGCAGAGGACTGCGGCCCGGGGAAGAGCAACGGGCGCCTGCACAAAGCG    60
Qy  1331  GGCGCCTGTCGGTGCTGGTGGAGTGCGGCCATGTACGCGCGGCCGGGCGCCTGCTG  1390
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  GGCGCTGTCGGTGCTGGTGGAGTGCCATGTACGCG--AGGCCTTCTCGTCTGGGTTGCGGTGCTG  118
Qy  1391  CAGCGACGAGGCGGCGCAGCACACTGCACGACAACCCGCCGAAACTCCTGCGAGGACAC  1450
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   119  CAGCGACGAGGCGGCGCA--ACAGCACCTGCACGAGAACACCCGCCGAAACTGCTGCGAGGACAC  176
Qy  1451  CGTGTACAGGAGGAGCGGGGTTGATGACCGAGGTAGAGAAAAACGTCTCCGAGAAGGGGAG  1510
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   177  CGTGTACAGGAGGAGCGGGGTTGATGACCGAGGTAGAGAAAAACGTCTCCGAGAAGGGGAG  236
Qy  1511  GAGGATCATGTACG-CCCGGAGTAGGACACCTCGTCGTCAGTCGTCGTCTGGGGTTTGGGCCGCAG  1569
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   237  GAGGATCATGTACGCCCCGGAGTAGGACCTCGTCCAGTCGTTCCTTGGGTTTGGGCCGCAG  296
Qy  1570  CCATGA-TCCTCCGAANTCTGGTTGGGGCATCCAGCATACGGCCAAGTGCACAACAATCAGC  1628
          |||||||||||||||||||||||||||||||||||||||||||||
Db   297  CATTGATTCCTCCGAANCCTGGTTGGGGCATCCAGCATACGGCCAAGTGTCACAACAATCAGC  356
Qy  1629  CCTGGGCCAGACACGAGCGAGCAGG-AGGGAGAGACAGAGAAAAGAGAAGAAAACACAGCATGAGAACA  1687
          ||||||||||||||||||||||||||||||||||||||||||||
Db   357  CCTGGGCAGACACGAGCAGGAGCAGAGAAAGAGAAAGAAAACACAGCATGAGAGAACA  416
Qy  1688  CAGTAAATGAATAAAACCATAAAAATATTTAGCCCCCTCGTGTTCTGTTCTTACTGGCCAGGA  1747
          |||||||||||||||||||||||||||||||||||||||||||||
Db   417  CAGTAAATGAAT-AAACCATAAAATATTTAG--CCCTCGTGTTCTGTTGTGCNTACTGGNCAGGA  474
Qy  1748  AATGGTTACCAANTTTTCAGTGTTGGACTTGACAGCTTCTTTTTGGCCACAGACGAAGAGAGGAA  1807
          |||||||||||||||||||||||||||||||||||||||||||||
Db   475  AATGGTTACC-ANTTTTCAGTGTTTGACTTNACAGCTTCTTCTTTTGGCCAAGACGAAGAGAG-A  532
Qy  1808  TTTAACACTGTTTCAAACCCGGGG  1831
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Db   533  NTTAACACTGTTTCAAANCCGGGGG  556
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Right column

RESULT 10

US-09-867-701-4240/c

; Sequence 4240, Application US/09867701
; Patent No. US2002013237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; SOFTWARE: FastSEQ for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 10912
; SEQ ID NO 4240
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-4240

Query Match   20.9%;   Score 396.4;   DB 10;   Length 409;
Best Local Similarity 99.5%;   Pred. No. 2.3e-94;
Matches 408; Conservative   0; Mismatches   1; Indels   1; Gaps 1;

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Qy  1468  TGATGACCGAGCTGAGGTAGAAAAAACGTCTCCGAGAAGGGGAGGAGGAGGAGGATCAGTGTACCGCCC  1527
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Db   409  TGATGACCGAGCTGAGGTAGAAAAAACGTCTCCGAGAAGGGGAGGAGGAGGAGGATCAGTGTACCGCCC  350
Qy  1528  GGAAGTAGGACCTCGTCCCAGTCGTCGTCTTGTGGGTTTGGCCGCGGCCAGCCATGCCATGGAGAATCT  1587
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   349  GGAAGTAGGACCTCGTCCAGTCGTCGTTGTGGGTTT-GCCGCCAGCCATGAGATCCTTCCGGAATCT  291
Qy  1588  GGTTGGGCATCCAGCATACGGCCAATGTCACACAATCAGCCCCTGGGCCAGACACGACGAGCAG  1647
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Db   290  GGTTGGGCATCCAGCATACGGCCAATGTCACACAATCAGCCCCTGGGCCAGACACGACGAGCAG  231
Qy  1648  GAGGGAGAGACAGAGAAAAGAGAAAAAACAGCATGAGAACACAGTAAATGAATAAAAACCAT  1707
          ||||||||||||||||||||||||||||||||||||||||||||
Db   230  GAGGGAGAGACAGAGAAAAGAGAAAAAACAGCATGAGAACACAGTAAATGAATAAAAACCAT  171
Qy  1708  AAAAATATTTAGCCCCTCTGTGTTCTGTGTCCTTACTGGCCAGGAAATGGTTACCAATTTTTCAGT  1767
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Db   170  AAAATATTTAGCCCCTCTGTTCTGTGTCCTTACTGGCCAGGAAATGGTTACCAATTTTTCAGT  111
Qy  1768  GTTGGACTTGACAGCTTCTTTTGCCACAAGCAAGAAGAATTTAACACTGTTTCAAACCC  1827
          |||||||||||||||||||||||||||||||||||||||||||||
Db   110  GTTGGACTTGACAGCTTCTTTTGCCACAAGCAAGAAGAATTTAACACTGTTTCAAACCC  51
Qy  1828  GGGGGAGTTGGCTGTGTTGTTTAAAGAAAAGACCATTAAAATGCTTTAGACAGTGT  1877
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Db    50  GGGGGAGTTGGCTGTGTTGTTTAAAGAAAAGACCATTAAAATGCTTTAGACAGTGT  1
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RESULT 11

US-09-867-701-4251

; Sequence 4251, Application US/09867701
; Patent No. US2002013237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 4251
; LENGTH: 430
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-4251

Query Match   20.0%; Score 378.6; DB 10; Length 430;
Best Local Similarity   96.3%; Pred. No. 1.1e-89;
Matches 419; Conservative 1; Mismatches 10; Indels 5; Gaps 3;

Qy   524 TCCCCAGGGAAACTGAACTCAGTTTGCATCAGCTGCTGCGAACACCCCTCTTTGTAACGGG 583
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Db   1 TCCCCAGGGAAACTGAACTCAGTTTTGCATCAGCTGCTGCGAACACCCCTCTTTGTACGGGC 60

Qy   584 CCAAGGCCCAAGAAAAGGGGAAGTTCTGCCTCGGGCCCTCCGCACCACC 643
            |-||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CAAGG---CAAGAAAAGGGGAAGTTCTGCCTCGGGCCCTCAGG-CAGGGCTCCGCACCACC 116

Qy   644 ATCCTGTTCCTCAAATTAGCCCTCTTCTCTCGGGCACACTGCGTGAAGCTGAAGGAGATCCCAC 703
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   117 ATCCTGTTCCTCAAATTAGCCCTCTTCTCCGGCACACTGCGTGAAGCTGAAGGAGATGGCTC 176

Qy   704 CCCCTCCTGCATTGTTCTTCCCAGCCCCCCAACCCCCCGCCCCCGAGTGAGTTT 763
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   177 CCCGT-CTGCATTGTTCTTCCCAGCCCCCCAACCCCCCTGCCCCCTGAGTGAGTTT 235

Qy   764 CTTCTCGGGTGTCCTTTTATTCTGGGTAGGGAGGCGGGAGTCCGTGTGTTCTCTTTTTTGTTCCTG 823
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   236 CTTCTCGGGTGTCCTTTTATTCTGGGTAGGGAGGGGGGAGTCCGTGTGTTCTCTTTTTTGTTCCTG 295

Qy   824 TGCAAATAATGAAAGAGACTCGGTAAAGCATTCTGAATAAAATTCAGCYTGACTGAATTTTC 883
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   296 TGCAAAGCAATGAAAGAGCTCGGTAAAGACATTCTGAATAAAATTCAGCGTTGACTGAATTTTTC 355

Qy   884 AGTATGTACTTGAAGGAAGGAGGTGGAGTGAAGTTCACCCCCATGTTCTGTGTAACCGGA 943
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   356 AGTATGTACTTGAAGGAAGGAGGTGGAGTGAAAGTTCACCCACCATGTTCTGTGTAACCGGA 415

Qy   944 GTCAAGGCCCAGGCTG 958
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Db   416 GTCAAGGCCCAGGCTG 430

RESULT 12
US-09-825-294-9
; Sequence 9, Application US/09825294
; Patent No. US20020044911A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSEQ for Windows Version 3.0
;
SEQ ID NO 9
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-9

Query Match   19.4%; Score 368.8; DB 10; Length 396;
Best Local Similarity   97.2%; Pred. No. 3.8e-87;
Matches 385; Conservative 0; Mismatches 9; Indels 2; Gaps 1;

Qy   270 TAGGCATCGCGCGGCCAACTCTTTTGCGGATTGTGTTCTTGCTTCCAGGCTTTGCAAATCC 329
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Db   1 TCGACAATCGCGCGGCAACTTTTTTGCGGATTGTTCTTGCTTCCAGGCTTTGCAAATCC 60

Qy   330 AGTGCTACCAGTGTGAAGAAATTCCACTGACACAAGCACTGCTCTCCCCGAGTTCATTG 389
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Db   61 AGTGCTACCAGTGTGAAGAAATTCCACTGACACAATGTGTCAGAGAAGAAGCACTGCTCTCCCCGAGTTCATTG 120

Qy   390 TGAATTGCACGGTGAACGTTCAAGACAACATGTTGTCAGAAGAAGAAGTGATGGAGACAAAAGTGCCG 449
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TGAATTGCACGGTGAACGTTCAAGACAACATGTTGTCAGAAGAAGAAGTGATGGAGACAAAAGTCCG 180

Qy   450 GGATCATGTACCGCAAGTCCTGTGCATCATCAGCGCGGCCGCTGTCTGTCATGCCCCGGT 509
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Db   181 GGATCATGTACCGCAAGTCCTGTGCATCATCAGCGCGGCCGCTGTCTGTCATGCCCCGGT 240

Qy   510 ACCAGTCCTTCTGCTCCCCAGGGAAACTGAACTCAGTTTGCATCAGCTGCTGCGAACACC 569
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ACCAGTCCTTCTGCTCCCCAGGGAAACTGAACTCAGTTTGCATCAGCTGCTGCGAACACC 300

Qy   570 CTCTTTGTAACGGGCCAAGGCCCAAGAAAAGGGGAA--GTTCTGCCTCGGGCCCTCAGGC 627
            |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   301 CTCTTTGTAACGGGCCAAGGNCAAAAAAAGGGGAAAGTTCTGNCCTCGGGCCCTCAGGCC 360

Qy   628 AGGGCTCCGCACCACCATCCCTGTTCCTCAAAATTAGC 663
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Db   361 AGGGCTCCGCACCACCATCCTGTTCCTCAAAATTAGC 396

RESULT 13
US-09-825-294-199
; Sequence 199, Application US/09825294
; Patent No. US20020044911A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C5
; CURRENT APPLICATION NUMBER: US/09/825,294
; CURRENT FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FastSEQ for Windows Version 3.0
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SEQ ID NO 199
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(369)
; OTHER INFORMATION: n = A,T,C or G
US-09-825-294-199

Query Match   19.3%; Score 365.4; DB 10; Length 369;
Best Local Similarity   99.2%; Pred. No. 2.8e-86;
Matches 366; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy   280 GGCAACTTTTTGCGGATTGTTCTTGCTTCCAGGCGTTTGCGCCTGCAAATCCAGTGCTACCA 339
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Db   1 GGCAACTTTTTGCGGATTGTTCTTGCTTCCAGGCGTTTGCGCCTGCAAAATCCAGTGCTACCA 60

Qy   340 GTGTGAAGAAATTCCAGCTGAACAACGACTGCTCCTCCCCGAGTTCATTGTGAATTGCAC 399
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Qy   400 GGTGAACGTTCAAGACATGTTGTCAGAAGAAGAAGTGATGGAGACAAAAGTGCCGGGATCATGTA 459
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Db   121 GGTGAACGTTCAAGACATGTTGTCAGAAGAAGAAGTGATGGAGACAAAAGTGCCGGGATCATGTA 180

Qy   460 CCGCAAGTCCTGTGCATCATCAGCGCGGCCGCTCTGCGGGGTACCAGTCATGTA 519
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Qy   580 CGGGCCAAGGCCCAAGAAAAAGGGGAAGTTCTGCCTCGGCCTCAGGCGGCTCCGCAC 639
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Db   301 CGGGCCAAGGCCCAAGAAAAAGGGGAAGTTCTGCCTCGGCCTCAGGCGGCTCCGCAC 360

Qy   640 CACCATCCT 648
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RESULT 14
US-09-867-701-1516/c
; Sequence 1516, Application US/0986701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
;   APPLICANT: Aglate, Paul A.
;   APPLICANT: Jones, Robert
;   APPLICANT: Harlocker, Susan L.
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;   TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
;   FILE REFERENCE: 210121.497
;   CURRENT APPLICATION NUMBER: US/09/867,701
;   CURRENT FILING DATE: 2001-05-29
;   NUMBER OF SEQ ID NOS: 10912
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 1516
;   LENGTH: 373
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-867-701-1516

Query Match   19.1%;   Score 362; DB 10;   Length 373;
Best Local Similarity   99.7%;   Pred. No. 2.2e-85;
Matches   373; Conservative   0; Mismatches   0; Indels   1; Gaps   1;

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Qy  1504 AGGGGAGGAGGAGATCATGTACGCCCGGAAGTAGAGACCTCGTCCAGTCGTCCTTGGGTTTGG 1563
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Db   373 AGGGGAGGAGGAGATCATGTACGCCCGGAAGTAGGAACCTCGTCCAGTCGTCCTTGGGTTT-G 1503

Qy  1564 CCGCAGGCCATGAATCCTCCGAATCTGGTTGGGCATCCAGCATACGGCCAAATGTCACACAA 1623
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Db   314 CCGCAGGCCATGAATCCTCCGAATCTGGTTGGGCATCCAGCATACGGCCAAATGTCACACAA 255

Qy  1624 TCAGCCCCTGGGCGGGACACAGCGAGGAGGAGGAGAAAAGACACAGCCATGAG 1683
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Qy  1684 AACACAGTAAATGAATAAAAAACCATAAAAATATTTAGCCCCTCTTACTTACTGCC 1743
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Db   194 AACACAGTAAATGAATAAAAAACCATAAAAATATTTAGCCCCTCTTACTTACTGCC 135

Qy  1744 AGGAAATGGTACCAATTTTTCAGTGTGTTGGACTTGACAGCTTC-T 1803
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Db   134 AGGAAATGGTACCAATTTTTCAGTGTGTTGGACTTGACAGCTTC 75

Qy  1804 AGAATTTAACACTGTTTCAAACCCGGGGGGAGTTGGCTGTGTTA 1863
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Db    74 AGAATTTAACACTGTTTCAAACCCGGGGGGAGTTGGCTGTGTTA 15

Qy  1864 GCTTTAGACACGTGT 1877
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RESULT 15
US-09-867-701-1532
; Sequence 1532, Application US/0986701
; Patent No. US20020132237A1

; GENERAL INFORMATION:
;   APPLICANT: Aglate, Paul A.
;   APPLICANT: Jones, Robert
;   APPLICANT: Harlocker, Susan L.
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;   TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
;   FILE REFERENCE: 210121.497
;   CURRENT APPLICATION NUMBER: US/09/867,701
;   CURRENT FILING DATE: 2001-05-29
;   NUMBER OF SEQ ID NOS: 10912
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 1532
;   LENGTH: 390
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(390)
;   OTHER INFORMATION: n = A,T,C or G
US-09-867-701-1532

Query Match   18.7%;   Score 354; DB 10;   Length 390;
Best Local Similarity   98.7%;   Pred. No. 2.8e-83;
Matches   387; Conservative   0; Mismatches   2; Indels   3; Gaps   3;

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Qy  1488 AAAAACGTCTCCGAGAAGGGGAGGAGGAGATCATGTACGCCCCGGAAGTAGGAACCTCGTCCAG 1547
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Qy  1548 TCGTGCTTGGGTTTGGCGCGCAGCCATGAATCCTCCGAATCTGGTTGGGCATCCAGCATACG 1607
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Qy  1608 GCCAAATGTCACAACAATCACCCCTGGGCAGACACACGAGCAGGAGGAGGAGAGAGAAAAG 1667
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Qy  1668 AAAAACACAGCCATGAGAAACACAGTAAATGAATAAAAAACCATAAAAATATTTAGCCCCTCTGT 1727
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Qy  1787 TTTTGCCACAAGCACAAGAGAGAATTTAACACTGTTTCAAACCCGGGGGGAGTTGGCTGTGTTA 1846
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Qy  1847 AAGAAAGACCATTAAATGCTTTAGACAGTGTA 1878
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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SUMMARIES

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5	1873	98.7	1967	1	PCT-US02-29964-16	Sequence 16, App1
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9	1863.2	98.2	1925	25	US-09-652-128-9375	Sequence 9375, Ap
10	1863.2	98.2	1925	25	US-09-699-997-111085	Sequence 11085, A
11	1863.2	98.2	1925	27	US-09-652-917-3346	Sequence 3346, Ap
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13	1863.2	98.2	1925	29	US-09-726-805-1608	Sequence 1608, Ap
14	1851	97.6	1917	17	US-09-371-168-7188	Sequence 7188, Ap
15	1851	97.6	1917	25	US-09-644-873-9077	Sequence 9077, Ap
16	1851	97.6	1917	25	US-09-652-109-9370	Sequence 9370, Ap
17	1851	97.6	1917	25	US-09-652-121-6191	Sequence 6191, Ap
18	1851	97.6	1917	25	US-09-652-128-7518	Sequence 7518, Ap
19	1851	97.6	1917	25	US-09-652-355-9112	Sequence 9112, Ap
20	1851	97.6	1917	25	US-09-652-914-8473	Sequence 8473, Ap
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c	27	1845.8	97.3	1956	40	US-10-105-083-1915	Sequence 1915, Ap
c	28	1845.8	97.3	1956	40	US-10-105-299-2415	Sequence 2415, Ap
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c	30	1526	90.9	1832	40	US-10-108-260A-197	Sequence 197, Ap
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	33	1606.2	84.7	1619	28	US-09-713-550-205	Sequence 205, App
	34	1606.2	84.7	1619	31	US-09-825-294-205	Sequence 205, App
	35	1606.2	84.7	1619	31	US-09-825-294-211	Sequence 211, App
	36	1606.2	84.7	1619	31	US-09-970-966-205	Sequence 205, App
	37	1606.2	84.7	1619	36	US-09-970-966-211	Sequence 211, App
	38	1606.2	84.7	1619	36	US-09-970-966-205	Sequence 205, App
	39	1606.2	84.7	1619	42	US-10-212-677-205	Sequence 205, App
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	41	1570	82.8	2573	76	US-60-324-185-14798	Sequence 14798, A
	42	1557.4	82.1	2521	61	US-60-172-373-2499	Sequence 2499, Ap
	43	1523.2	80.3	1524	40	US-10-119-480-15	Sequence 15, Appl
	44	1523.2	80.3	1524	42	US-10-216-159A-15	Sequence 15, Appl
	45	1523.2	80.3	1524	42	US-10-216-160-15	Sequence 15, Appl

RESULT 1
PCT-US01-45395-214
Sequence 214, Application PCT/US0145395
GENERAL INFORMATION:
APPLICANT: Corixa Corporation
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Molesh, David Alan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.48401PC
CURRENT APPLICATION NUMBER: PCT/US01/45395
CURRENT FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 214
LENGTH: 1897
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US01-45395-214

Query Match   100.0%;   Score 1896.2;   DB 1;   Length 1897;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 1897;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

ALIGNMENTS

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Qy    1  GCCAACTCCGGAGGCTCTGGTGCTGCTCGGCCCCGGGAGCCGCGGAGGAGCAGAGACCCG   60
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Db    1  GCCAACTCCGGAGGCTCTGGTGCTGCTCGGCCCCGGGAGCCGCGGAGGAGCAGAGACCCG   60

Qy   61  CAGCCGGGAGCCCGGGCGATCAGAGGTTCCGGAGCGGCGCACTGCGGGTCCTCCTCTA  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  CAGCCGGGAGCCCGGGCGATCAGAGGTTCCGGAGCGGCGCACTGCGGGTCCTCCTCTA  120

Qy  121  AGCTACGACCGTCGTCTCCGCGCGGCCGAGCCCTCGGCTCGGCTCGGTCTCCTCGGGCACAATC  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  AGCTACGACCGTCGTCTCCGCGCGGCCGAGCCCTCGGCTCGGCTCGGTCTCCTCGGGCACAATC  180

Qy  181  CGCTGCAGCCGGGGGCAGCAGCCTCGTGTCGCCGCCGCGGCAACTTTTTGCGGGT...  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  CGCTGCAGCCGGGGGCAGCAGCCTCGTGTCGCCGCCGCGGCAACTTTTTGCGGGT...  240

Qy  241  GCCCCGGGACTCCGGGAGAAATGTGGGTCCTAGGCATCGCGGCAACTTTTTGCGGATTGTT  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  GCCCCGGGACTCCGGGAGAAATGTGGGTCCTAGGCATCGCGGCAACTTTTTGCGGATTGTT  300

Qy  301  CTTGCTTCCAGGCTTTCGCGCTTGCAAATCCAGTTGCTACCAGTGTGAAAGAAATTCAGCTGAA  360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  CTTGCTTCCAGGCTTTCGCGCTTGCAAATCCAGTTGCTACCAGTGTGAAAGAAATTCAGCTGAA  360

Qy  361  CAACGACTAGTGCTCCTCCCCGAGTTCATTGTGAATTGCACGGTGGTGAACGTTCAAGACACATGTG  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  CAACGACTAGTGCTCCTCCCCGAGTTCATTGTGAATTGCACGGTGGTGAACGTTCAAGACACATGTG  420

Qy  421  TCAGAAAGAAAGTGAATGAGCAAAAGTGCGGGATCATGTACCGCAAGTGTCTGTGCATCATC  480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  TCAGAAAGAAAGTGAATGAGCAAAAGTGCGGGATCATGTACCGCAAGTGTCTGTGCATCATC  480

Qy  481  AGGGGCCGTTGTCCCAGTCTCTCTCGCCGCCTGTTTCTCCTGCCAGGGAAACTGAA  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481  AGGGGCCGTTGTCCCAGTCTCTCTCGCCGCCTGTTTCTCCTGCCAGGGAAACTGAA  540

Qy  541  CTCAGTTTGCATCAGCTGCTGCAACACCCCTCTTTTGTTAACGGGCCCAAAGAAAAG  600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541  CTCAGTTTGCATCAGCTGCTGCAACACCCCTCTTTTGTTAACGGGCCCAAAGAAAAG  600

Qy  601  GGGAAGTTCTGCCCTCGGCCCCTCAGGCCACCAGGCTCCGCCACCAACATCCTGTTCCTCAAATT  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601  GGGAAGTTCTGCCCTCGGCCCCTCAGGCCACCAGGCTCCGCCACCAACATCCTGTTCCTCAAATT  660

Qy  661  AGCCCTCTTCTCTCGGCACACTGTCTGAAGCTGAAGGAGAAGATGCCACCCCTCCTGCATTGTTC  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661  AGCCCTCTTCTCTCGGCACACTGTCTGAAGCTGAAGGAGAAGATGCCACCCCTCCTGCATTGTTC  720

Qy  721  TTCCAGCCCTTGCGCCCCAACCCCACCCCTCCCTGAGTGAGTTTCTTCTTTGGGTGTTCCTTTT  780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721  TTCCAGCCCTTGCGCCCCAACCCCACCCCTCCCTGAGTGAGTTTCTTCTTTGGGTGTTCCTTTT  780

Qy  781  ATTCTTGGGTTAGGGAGGACCGGGAGTCCGTTGTTCTCTTTTGGTGTTCCTGTTCCAAATAATAATGAAAAGAG  840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781  ATTCTTGGGTTAGGGAGGACCGGGAGTCCGTTGTTCTCTTTTGGTGTTCCTGTTCCAAATAATAATGAAAAGAG  840

Qy  841  CTCCGTAAAGCATTCTGAATAAATTCAGCYTGACTGAAGTTTCAGTGAATGTTGAAGGA  900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841  CTCCGTAAAGCATTCTGAATAAATTCAGCYTGACTGAAGTTTCAGTGAATGTTGAAGGA  900

Qy  901  AGGAGGTGGAGTGAAAGTTCACCGGAGTCAAGGCCAGGCTGGC  960
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Db  901  AGGAGGTGGAGTGAAAGTTCACCGGAGTCAAGGCCAGGCTGGC  960

Qy  961  AGAGTCWGTCCTTAGAAGTCACTGAGGTGGGCATCTGCCTTTTGTAAAGCCTCCAGTGTC  1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961  AGAGTCWGTCCTTAGAAGTCACTGAGGTGGGCATCTGCCTTTTGTAAAGCCTCCAGTGTC  1020

Qy 1021  CATTCCATCCCTGATGGGGGGGCATAGTTGAGACTGAGAGTGAGAGTGAGAGGTTTCTTAG  1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021  CATTCCATCCCTGATGGGGGGGCATAGTTGAGACTGAGAGTGAGAGTGAGAGGTTTCTTAG  1080

Qy 1081  GGCTGGAGGGCCAGTTCCCACTCAAGGCTCCCGCTTGACATTCAAACTTCATCGTCTCCT  1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081  GGCTGGAGGGCCAGTTCCCACTCAAGGCTCCCGCTTGACATTCAAACTTCATCGTCTCCT  1140

Qy 1141  GAAAACCATTCTCTTCGCAGCAGAAATTGGCTGTTCGCGGTCTCAGTGACT  1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141  GAAAACCATTCTCTTCGCAGCAGAAATTGGCTGTTCGCGGTCTCAGTGACT  1200

Qy 1201  CGAGACTCAATGACTGGACTTAGACTGGGGCTCGGCCTCGGCTTGAAAAAGTGCTTAAGA  1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201  CGAGACTCAATGACTGGACTTAGACTGGGGCTCGGCCTCGGCTTGAAAAAGTGCTTAAGA  1260

Qy 1261  AAATCTTTCTCAGTTCTTCCTTGCAGAGGACTGGCGGCGAAGCAAACGGGCGCGCT  1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261  AAATCTTTCTCAGTTCTTCCTTGCAGAGGACTGGCGGCGAAGCAAACGGGCGCGCT  1320

Qy 1321  GCACAAAGCGGGCGCGTGTCGGTGGGAGTGCGCATGTAGGCGCAGGCGCGTTCTGTGGT  1380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    61 CACCCGGGAGCCCGAGCGCGGGCCGATGCGACGGCTCCGCGAGCGACGGCGCACCTGCGGCCTCCTCTA 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 GCCAACTCCGGAGGCTCGGTGCTCGGCGCCGAGCCGAGCAGGCGAGAGACCCG 60
Db     1 GCCAACTCCGGAGGCTCGGTGCTCGGCGCCGAGCCGAGCAGGCGAGAGACCCG 60
Qy     1 GCCAACTCCGGAGGCTCTGGTGCTCGGCGCCGGGGACGCGAGGCGAGGAGACCCG 60
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Query Match   100.0%; Score 1896.2; DB 31; Length 1897;
Best Local Similarity   100.0%;
Matches 1897; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

US-09-825-294-214
    LENGTH: 1897
    TYPE: DNA
    ORGANISM: Homo sapiens
    FEATURE:
    NAME/KEY: misc_feature
    LOCATION: (1)..(1897)
    OTHER INFORMATION: n = A,T,C or G
SEQ ID NO 214
SOFTWARE: FastSEQ for Windows Version 3.0
NUMBER OF SEQ ID NOS: 215
CURRENT FILING DATE: 2001-04-03
CURRENT APPLICATION NUMBER: US/09/825,294
FILE REFERENCE: 210121.48405
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
APPLICANT: Fling, Steven P.
APPLICANT: Algate, Paul A.
APPLICANT: Stolk, John A.
APPLICANT: Xu, Jiangchun
GENERAL INFORMATION:
Sequence 214, Application US/09825294
US-09-825-294-214

RESULT 2

GENERAL INFORMATION:
APPLICANT: Stolk, John A.
APPLICANT: Molesh, David Alan
APPLICANT: Fling, Steven P.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C6
CURRENT APPLICATION NUMBER: US/09/970,966
CURRENT FILING DATE: 2001-10-02
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 214
LENGTH: 1897
TYPE: DNA
ORGANISM: Homo sapiens
US-09-970-966-214

Query Match   100.0%;   Score 1896.2;   DB 36;   Length 1897;

RESULT 3
US-09-970-966-214
Sequence 214, Application US/0970966
US-09-970-966-214

Best Local Similarity 100.0%;
Matches 1897;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;   Pred. No. 0;

Qy   1 GCCAACTCGGGAGCCTGCTCTTGGTGCTCGGCGCCCGCCCGGAGACGCGAGAGACCCG   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GCCAACTCGGGAGCCTGCTCTTGGTGCTCGGCGCCCGCCCGGAGACGCGAGAGACCCG   60

Qy   61 CAGCCGGGGAGCCCGAGCCGGCGATGCAGGCTCCGGGAGGCGGCCACCTGCCTCTCTA 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CAGCCGGGGAGCCCGAGCCGGCGATGCAGGCTCCGGGAGGCGGCCACCTGCCTCTCTA 120

Qy   121 AGCTACGACCGTGTCTCCCGGGCAGCAGGGCCCAGCAGCGCCTCGGCCCAGCCAGC   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AGCTACGACCGTGTCTCCCGGGCAGCAGGGCCCAGCAGCGCCTCGGCCCAGCCAGC   180

Qy   181 CGCTGCAGCGCGGGGGCCTCCCGGGGGCTGCCCCTGTCCCCTCTCCCG   240
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CGCTGCAGCGCGGGGGCCTCCCGGGGGCTGCCCCTGTCCCCTCTCCCG   240

Qy   241 GCCCCGGGGACTCCGGGAGAAATGTGGGTCCTAGGCATCGGGGATTGTT   300
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GCCCCGGGGACTCCGGGAGAAATGTGGGTCCTAGGCATCGGGGATTGTT   300

Qy   301 CTTGCTTCCAGGCTTTGCGGCTGCAAATCCAGTGCTACCAGTGTGAAGAATTCCAGCTGAA 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTTGCTTCCAGGCTTTGCGGCTGCAAATCCAGTGCTACCAGTGTGAAGAATTCCAGCTGAA 360

Qy   361 CAACGACTGCTCCTCCCCCGAGTTCATTGTGAATGCACGGTGAACGTTCAAGACATGTG   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CAACGACTGCTCCTCCCCCGAGTTCATTGTGAATGCACGGTGAACGTTCAAGACATGTG   420

Qy   421 TCAGAAAGAAGTGAGTGCCGGGCAAAGTGCCGGGGATCATGTACCGGCGAGTCCGTGCATCATC 480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TCAGAAAGAAGTGAGTGCCGGGCAAAGTGCCGGGGATCATGTACCGGCGAGTCCGTGCATCATC 480

Qy   481 AGCGGCCTGTCTCATCGCCTCTGCGGGTACCAGTCCTTCTGCTCCCCCAGGGAAACTGAA   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AGCGGCCTGTCTCATCGCCTCTGCGGGTACCAGTCCTTCTGCTCCCCCAGGGAAACTGAA   540

Qy   541 CTCAGTTTGCATCAGCTGCTGCAAACACCCCTCTTTGTTGTAAGGGCCCAAGGCCCAAGAAAG 600
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CTCAGTTTGCATCAGCTGCTGCAAACACCCCTCTTTGTTGTAAGGGCCCAAGGCCCAAGAAAG 600

Qy   601 GGGAAGTTCTGCCCTCCGGCCCTCCGCCACCAACCATCCTGTTCCTCAAATT   660
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GGGAAGTTCTGCCCTCCGGCCCTCCGCCACCAACCATCCTGTTCCTCAAATT   660

Qy   661 AGCCCTCTTCTCTCGGCACACTGCTGAAGGCTGAAGGAGGAGGAATGCCACCCCTCCTGCAATTGTTC   720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGCCCTCTTCTCTCGGCACACTGCTGAAGGCTGAAGGAGGAGGAATGCCACCCCTCCTGCAATTGTTC   720

Qy   721 TTCCAGCCCTTGCGCCCCCAACCCTCCCTGAGTGAGTTCTTCTTCGGGTGTCCTTTTT   780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 TTCCAGCCCTTGCGCCCCCAACCCTCCCTGAGTGAGTTCTTCTTCGGGTGTCCTTTTT   780

Qy   781 ATTCTGGGTAGGGAGCGGGGACTCCGTGGTTCTCTTTTTGTTCCTGTGTGCAAAATAATGAAAGAG   840
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 ATTCTGGGTAGGGAGCGGGGACTCCGTGGTTCTCTTTTTGTTCCTGTGTGCAAAATAATGAAAGAG   840

Qy   841 CTCGGTAAAGCATTCTGAATAAATTCAGCYTGACTGAAATTTTCAGTATGTACTTGAAGGA   900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 CTCGGTAAAGCATTCTGAATAAATTCAGCYTGACTGAAATTTTCAGTATGTACTTGAAGGA   900

Qy   901 AGGAGGTGGAGTGAAAGTTCACCCCCATGTCTGTGTTGTAACCGGAGTCAAGGCCAGGCTGGGC   960
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 AGGAGGTGGAGTGAAAGTTCACCCCCATGTCTGTGTTGTAACCGGAGTCAAGGCCAGGCTGGGC   960

Qy   961 AGAGTCWGTCCTTAGAAGTCACTGAGGTGGGCATCTGCCTTTTGTAAAGCCTCAGTGTC 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 AGAGTCWGTCCTTAGAAGTCACTGAGGTGGGCATCTGCCTTTTGTAAAGCCTCAGTGTC 1020

Qy   1021 CATTCCATCCCTGATGGGGGCCATAGTTTGAGACTGCAGAGTGAGAGTGAGTTTCTTAG 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   1141 GAAAACCATTCTCTGCAGCAGAATTGGCTGTGGTTTCCGCCGCCCTCGAGTTGGGTGGGCTCTAGTGACT
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GAAAACCATTCTCTGCAGCAGAATTGGCTGTGGTTTCCGCCGCCCTCGAGTTGGGTGGGCTCTAGTGACT

Qy   1201 CGAGACTCAATGACTGGGACTTAGACTGGGCTTCGGCGCTCCGGCTCTTGCTTCTCTGAAAAGTTGCTTAAGA 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CGAGACTCAATGACTGGGACTTAGACTGGGCTTCGGCGCTCCGGCTCTTGCTTCTCTGAAAAGTTGCTTAAGA 1260

Qy   1261 AAATCTTCTCAGTTCTCCTTTGCAGAGAGACTGCCGCTGGGGCCGCCCT 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 AAATCTTCTCAGTTCTCCTTTGCAGAGAGACTGCCGCTGGGGCCGCCCTA 1320

Qy   1321 GCACAAAGCGGGCGGCGTCGTCGGTGGGTGGGTGGGAGTGCGGGCGGCTTCGTCGTGGT 1380
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GCACAAAGCGGGCGGCGTCGTCGGTGGGTGGGTGGGAGTGCGGGCGGCTTCGTCGTGGT 1380

Qy   1381 TGGCGTGCTTGCACGGACGAGGGGGGCCAGCAGCACACCCCGCCGAAAACTGCT 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TGGCGTGCTTGCACGGACGAGGGGGGCCAGCAGCACACCCCGCCGAAAACTGCT 1440

Qy   1441 GCGAGGACACCCGTGTACAGGACGGGGTTGATGACCGTGAGGTAGTAGAAAAAACGTCTCCG 1500
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GCGAGGACACCCGTGTACAGGACGGGGTTGATGACCGTGAGGTAGTAGAAAAAACGTCTCCG 1500

Qy   1501 AGAAGGGGAGGAGGATCATGTACGCCCGGGACTAGGACCTCCAGTCGTGCTTGGGGTT 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGAAGGGGAGGAGGATCATGTACGCCCGGGACTAGGACCTCCAGTCGTGCTTGGGGTT 1560

Qy   1561 TGGCCGCAGCCATGATCCTCCGAATCTGGTTGGGCATCCAGCATACGGCGAAATGTCACAA 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TGGCCGCAGCCATGATCCTCCGAATCTGGTTGGGCATCCAGCATACGGCGAAATGTCACAA 1620

Qy   1621 CAATCACCCCTGGGCACACACGACGAGGAGAGAGAAAAAAACACAGCAT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CAATCACCCCTGGGCACACACGACGAGGAGAGAGAAAAAAACACAGCAT 1680

Qy   1681 GAGAAACACAGTAAAATGAATAAAACCATAAAATATTTAGCCCCTCTGTTCTCTTACTG 1740
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GAGAAACACAGTAAAATGAATAAAACCATAAAATATTTAGCCCCTCTGTTCTCTTACTG 1740

Qy   1741 GCCAGGAAATGGTACCAATTTTTCACGTGTTGGACGAGCTTCTTTTGTTGCCACAGCAA 1800
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCCAGGAAATGGTACCAATTTTTCACGTGTTGGACGAGCTTCTTTTGTTGCCACAGCAA 1800

Qy   1801 GAGAGAATTTAACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTGTTAAAGAAGACCATTA 1860
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GAGAGAATTTAACACTGTTTCAAAACCCGGGGGAGTTGGCTGTGTGTTAAAGAAGACCATTA 1860

Qy   1861 AATGCTTTAGACAGTGTAAAAAAAAAAAAAAAAAAAA 1897
             |||||||||||||||||||||||||||||||||||||
Db   1861 AATGCTTTAGACAGTGTAAAAAAAAAAAAAAAAAAAA 1897

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Db   1021 CATTCCATCCTGATGGGGGGCATAGTTTGAGACTGAGAGTGACGTTTCTTAG 1080
Qy   1081 GGCTGGAGGGCCAGTTCCCACTCAAGGCTCCTCCTTGACATTCAAACTTCATGCTCCT 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGCTGGAGGGCCAGTTCCCACTCAAGGCTCCTCCTTGACATTCAAACTTCATGCTCCT 1140
Qy   1141 GAAAACCAATTCTCTGCAGAGAATTGGCGTCGTTTCGCGCCTGAGTTGGGCTCTAGTGACT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GAAAACCAATTCTCTGCAGAGAATTGGCGTCGTTTCGCGCCTGAGTTGGGCTCTAGTGACT 1200
Qy   1201 CGAGACTCAATGACTGGGACTTAGACTGGGGCCTCGGCCCTCGTCTCGAAAAGTGCTTAAGA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CGAGACTCAATGACTGGGACTTAGACTGGGGCCTCGGCCCTCGTCTCGAAAAGTGCTTAAGA 1260
Qy   1261 AAATCTTCTCAGTTCTCCTTGCAGAGGACTTGGCGTCTCGGGCGGGGTTCGCGGGTCCTCTA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 AAATCTTCTCAGTTCTCCTTGCAGAGGACTTGGCGTCTCGGGCGGGGTTCGCGGGTCCTCTA 1320
Qy   1321 GCACAAAACGGGGGCCTGTGTCGGGTGGTGGGAGTGGGCATGGTACGGCGCCACCTGCGCCTCCTA 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GCACAAAACGGGGGCCTGTGTCGGGTGGTGGGAGTGGGCATGGTACGGCGCCACCTGCGCCTCCTA 1380
Qy   1381 TGGCGTGCTTGCTCAGGGACAGGGGCAGCAGCAACACCACCTGCGGCGAAACTGCTTAAGGTT 1440
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Db   1381 TGGCGTGCTTGCTCAGGGACAGGGGCAGCAGCAACACCACCTGCGGCGAAACTGCTTAAGGTT 1440
Qy   1441 GCGAGGACACCGTGTACAGGAGCGGGTTGATGACCGAGCTGAGGTAGAAAACGTCTCCG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GCGAGGACACCGTGTACAGGAGCGGGTTGATGACCGAGCTGAGGTAGAAAACGTCTCCG 1500
Qy   1501 AGAAGGGGAGGAGGGGATCAGTAGTACCCCGGGAAGTAGGACTCGTCGTGCTTGGGGTT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGAAGGGGAGGAGGGGATCAGTAGTACCCCGGGAAGTAGGACTCGTCGTGCTTGGGGTT 1560
Qy   1561 TGGCCGCAGCCATGATCATCCTCCGGAATCTGGTTGGGCCATCACCATACGGCCCAATGTCACAA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TGGCCGCAGCCATGATCATCCTCCGGAATCTGGTTGGGCCATCACCATACGGCCCAATGTCACAA 1620
Qy   1621 CAATCAGCCCTGGGCACACGAGCGGGTTGAGTGTAGCTGAGGTTCATTGTGAAATTCAAGACATGT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CAATCAGCCCTGGGCACACGAGCGGGTTGAGTGTAGCTGAGGTTCATTGTGAAATTCAAGACAT 1680
Qy   1681 GAGAACACAGTAAATGAATAAAAACCATAAAAAATATTTAGCCCTCCGTCTTGTTCTTGTGCTTACTG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GAGAACACAGTAAATGAATAAAAACCATAAAAAATATTTAGCCCTCCGTCTTGTTCTTGTGCTTACTG 1740
Qy   1741 GCCAGGAAATGGTACCAATTTTTCAGTGTTGGACTTGACAGCTTCTTTTGCCACAAGCAA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GCCAGGAAATGGTACCAATTTTTCAGTGTTGGACTTGACAGCTTCTTTTGCCACAAGCAA 1800
Qy   1801 GAGAGAATTTAACACTGTTTCAAACCCGGGGGACTTGGCGTGCTGTGTGTTTAAAGAAAGACCATTA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GAGAGAATTTAACACTGTTTCAAACCCGGGGGACTTGGCGTGCTGTGTGTTTAAAGAAAGACCATTA 1860
Qy   1861 AATGCTTTAGACAGTGTAAAAAAAAAAAAAAAAAAAAA 1897
          |||||||||||||||||||||||||||||||||||
Db   1861 AATGCTTTAGACAGTGTAAAAAAAAAAAAAAAAAAAAA 1897
```

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Qy      1 GCCAACTCCGGAGGGTCTGGTGTCTCGCGCCCGAGGGGAGGAGGACCCG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCCAACTCCGGAGGGTCTGGTGTCTCGCGCCCGAGGGGAGGAGGACCCG 60
Qy     61 CAGCGCCGGGAGCCCCGACGCGGCGGCCGGCGGGCTCCGGAGCCGCTCCCG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CAGCGCCGGGAGCCCCGACGCGGCGGCCGGCGGGCTCCGGAGCCGCTCCCTA 120
Qy    121 AGCTACGACACCGTCGTCTCCGGGGGCCAGCAGGGGCCCCAGCAGCGCCGGCAGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGCTACGACACCGTCGTCTCCGGGGGCCAGCAGGGGCCCCAGCAGCCAGC 180
Qy    181 CGCTGCAGCCGGGGCAGCCCTCCGCTCTGTGCCCTCTCTGATGCGGCCGTTCCCCG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CGCTGCAGCCGGGGCAGCCCTCCGCTCTGTGCCCTCTCTGATGCGGCCGTTCCCCG 240
Qy    241 GCCCCGGGGACTCCGGGGAGAATGTGGGGTCCAGGCATCGGGCCGGAAGCTCCAGG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GCCCCGGGGACTCCGGGGAGAATGTGGGGTCCAGGCATCGGGCCGGAAGCTCCAGG 300
Qy    301 CTTGCCTCCAGGCTTTGCGCTGCAAATCCAGTGCTACCAGTGTGAAGAATTCCAGCTGAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTTGCCTCCAGGCTTTGCGCTGCAAATCCAGTGCTACCAGTGTGAAGAATTCCAGCTGAA 360
Qy    361 CAACGACTGCTCCTCCCGAGTTCATTGTGAAGCGTGAACGTTCAAGACATGTG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAACGACTGCTCCTCCCGAGTTCATTGTGAAGCGTGAACGTTCAAGACATGTG 420
Qy    421 TCAGAAAGAAGTGATTGGGAGACAAAGTGCCGGGATCATGTACCGGCAAGTCCTGTCATCATC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TCAGAAAGAAGTGATTGGGAGACAAAGTGCCGGGATCATGTACCGGCAAGTCCTGTCATCATC 480
Qy    481 AGCCGCGCCTGTCTCATCGCCCTCTGCGCCCTGCACCTGCCTCTTCGCCTCTTCGCTCCATTGCGCAGAACTGAA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AGCCGCGCCTGTCTCATCGCCCTCTGCGCCCTGCACCTGCCTCTTCGCCTCTTCGCTCCAGGGAAACTGAA 540
Qy    541 CTCAGTTTGCATCAGCTGCTGCAAACACCCCTCTTTGTTGTAAACGGGCCAAGGCAAAAG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CTCAGTTTGCATCAGCTGCTGCAAACACCCCTCTTTGTTGTAAACGGGCCAAGGCAAAAG 600
Qy    601 GGGAAGTTCTGCCTCGGCCCCTCAGGCCGGCCAGGCCGCACCAACTCCTGTTCCTCAAATT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGGAAGTTCTGCCTCGGCCCCTCAGGCCGGCCAGGCCGCACCAACTCCTGTTCCTCAAATT 660
Qy    661 AGCCCTCTTCTCGGCCACACTGCTGAAGCTGAAGGAGAGGAGGACAACCCCTCCTGCATTGTTC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGCCCTCTTCTCGGCCACACTGCTGAAGCTGAAGGAGAGGAGGACAACCCCTCCTGCATTGTTC 720
Qy    721 TTCCAGCCCTTCGCCCCCAACCCCACCTCCCTGAGTGAGTTTTCTTCTGGTGTTCTTTT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TTCCAGCCCTTCGCCCCCAACCCCACCTCCCTGAGTGAGTTTTCTTCTGGTGTTCTTTT 780
Qy    781 ATTCTGGGTAGGGACCGGGAGTCCGGTGTCTGTTTCTCTGTTGCAAATAATGAAGAG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ATTCTGGGTAGGGACCGGGAGTCCGGTGTCTGTTTCTCTGTTGCAAATAATGAAGAG 840
Qy    841 CTCCGGTAAAGCATTCGAATAAAATCAGCYTGACTGAATTTGACTYGACTTGAAGGA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CTCCGGTAAAGCATTCTGAATAAATTCAGCYTGACTGAATTTCAGTRATGTACTTGAAGGA 900
Qy    901 AGGAGGTGGAGTGAAAGTTCACCCCCATGTCTGTGTTGTAACCGGAGTCAAAGGCCAGGCTGGC 960
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Db   901  AGGAGGTTGGGAGTGAAAAGTTCACCCCCATTGTGTGTAACCCGGAGTCAAGGCTTCCAGCTGGC  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   961  AGAGTCWGTCCTTAGAAGTCACTGAGGTGGGGCCATCTGCCTTTTGTAAAGCCTCCAGTGTC     1020

Db   961  AGAGTCWGTCCTTAGAAGTCACTGAGGTGGGGCCATCTGCCTTTTGTAAAGCCTCCAGTGTC     1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1021  CATTCCAATCCCTGATGGGGGGCATAGTAGTTTGACGAGTGAGAGTGACGTTTTCTTAG      1080

Db  1021  CATTCCAATCCCTGATGGGGGGCATAGTAGTTTGACGAGTGAGAGTGACGTTTTCTTAG      1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1081  GGCTGAGGGGGCCAGTTCCCACTCACTCAAGGCTCCTCCTCGCTTGACATTCAAACTTCATGCTCCT  1140

Db  1081  GGCTGAGGGGGCCAGTTCCCACTCACTCAAGGCTCCTCCTCGCTTGACATTCAAACTTCATGCTCCT  1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1141  GAAAACCATTCTCTGCAGCAGAAATTGGCTGTTTCCGCGCTTGACTTGGCTCTCAGTGACT    1200

Db  1141  GAAAACCATTCTCTGCAGCAGAAATTGGCTGTTTCCGCGCTTGACTTGGCTCTCAGTGACT    1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1201  CGAGACTCAAATGACTGGGGACTTAGACTGATGGGGGGCTCGGCCTCGCGTCTCGAAAAGTTGCTTAAGA 1260

Db  1201  CGAGACTCAAATGACTGGGGACTTAGACTGATGGGGGGCTCGGCCTCGCGTCTCGAAAAGTTGCTTAAGA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1261  AAATCTTCTCAGTTCTCCTTGCAGAGGACTGGCCGCGGGGACCGGAAGAGCAACGGGGCGGCT        1320

Db  1261  AAATCTTCTCAGTTCTCCTTGCAGAGGACTGGCCGCGGGGACCGGAAGAGCAACGGGGCGGCT        1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1321  GCACAAAAGCGGCGCGTGCGTGTTGGTCGGCATGTACCGCGCAGCGCGTTCTCTGTGGT         1380

Db  1321  GCACAAAAGCGGCGCGTGCGTGTTGGTCGGCATGTACCGCGCAGCGCGTTCTCTGTGGT         1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1381  TGGCGTGCTGCAGCGACAGGCGGCCAGCAGCAACACCCGGCGAAAACTGCT               1440

Db  1381  TGGCGTGCTGCAGCGACAGGCGGCCAGCAGCAACACCCGGCGAAAACTGCT               1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1441  GCGAGGACACCGTGTACAGAGAGACGGGTTGATGACCGGAGGTAGAAAAAACGTCTCCG        1500

Db  1441  GCGAGGACACCGTGTACAGAGAGACGGGTTGATGACCGGAGGTAGAAAAAACGTCTCCG        1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1501  AGAAGGGGGAGGGGGATCATGTGATACGGCCCGGGAAGTAGGAACCTTCGTCGTTCCTTGGGTT   1560

Db  1501  AGAAGGGGGAGGGGGATCATGTGATACGGCCCGGGAAGTAGGAACCTTCGTCGTTCCTTGGGTT   1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1561  TGGCCCGCAGCCATGATCCTCCGAAATCTGGTTGGGCAATCACGGCCAATGTCACAA           1620

Db  1561  TGGCCCGCAGCCATGATCCTCCGAAATCTGGTTGGGCAATCACGGCCAATGTCACAA           1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1621  CAATCAGCCCTGGGCAGAACGAGGCAGGAGGGAGAGAAAAGAAAAACACAGCCAT            1680

Db  1621  CAATCAGCCCTGGGCAGAACGAGGCAGGAGGGAGAGAAAAGAAAAACACAGCAT            1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1681  GAGAACACAGTAAATGAATAAAAACCATAAAAATATTTAGCCCCTCGTTCTCGTGCTTACTG     1740

Db  1681  GAGAACACAGTAAATGAATAAAAACCATAAAAATATTTAGCCCCTCGTTCTCGTGCTTACTG     1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1741  GCCAGGAAATGGTACCAAATTTTTCAGTGTTGGACTTGACAGCTTCTTTTGCCACAAGCAA      1800

Db  1741  GCCAGGAAATGGTACCAAATTTTTCAGTGTTGGACTTGACAGCTTCTTTTGCCACAAGCAA      1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1801  GAGAGAATTTAACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTGTTAAAGAAAGACCATTA    1860

Db  1801  GAGAGAATTTAACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTGTTAAAGAAAGACCATTA    1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1861  AATGCTTTAGACAGTGTAAAAAAAAAAAAAAAAAAAA 1897

Db  1861  AATGCTTTAGACAGTGTAAAAAAAAAAAAAAAAAAAA 1897
          |||||||||||||||||||||||||||||||||||||
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Query Match      98.7%;  Score 1873;  DB 1;  Length 1967;
Best Local Similarity   99.7%;  Pred. No. 0;
Matches 1884;  Conservative   2;  Mismatches   2;  Indels   1;  Gaps   1;

Qy    1  GCCAACTCCGGAGGCTCTGGTGCTCGGCCCGGGAGCCGCCGGAGGAGACCCCG   60
         ||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   80  GCCAACTCCGGAGGCGC--GGTGCTCGGCCCGGGAGCCGCCGGAGGAGACCCCG  138

Qy   61  CAGCCGGGGAGCCCGAGGCGCGGGGGCGGCGATGCAGGCTCCGCGACCTGCAGGCTCCTCTA  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  139  CAGCCGGGGAGCCCGAGGCGCGGGGGCGGCGATGCAGGCTCCGCGACCTGCAGGCTCCTCTA  198

Qy  121  AGCTACGACCGTCTCTCCCGCGGGCAGCAGCACCGCGGGCAGGCCTCGGCGCAGCCCACAGC  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  199  AGCTACGACCGTCGTCTCCCGCGGGCAGCAGCACCGCGGGCAGGCCTCGGCGCAGCCCACAGC  258

Qy  181  CGCTGCAGCCGCGGGGCAGCCTCCGCCGTCGCCCTGCGCTTGCCCTCTCCCG  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  259  CGCTGCAGCCGCGGGGCAGCCTCCGCCGTCGCCCTGCGCTTGCCCTCTCCCG  318

Qy  241  GCCCCGGGGACTCCGGGAGAATGTGGGTCCGGTCCGGTCGCAACTTTTTGCGGAGTTGTT  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          GCCCCGGGGACTCCGGGAGAATGTGGGTCCGGTCGCAACTTTTTGCGGAGTTGTT  300
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Db   319 GCCCCGGGGACTCCGGGAGAATGTGGGTCCTAGGCATCGCGGGATTGTT 378
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   301 CTTGCTTCCAGGGCTTTGCGCTTGCGCAAATCCAGTGCTACCAGTGTGAA 360
Db   379 CTTGCTTCCAGGGCTTTGCGCTTGCGCAAATCCAGTGCTACCAGTGTGAA 438
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   361 CAACGACTGCTTCCCCGAGTTCATTGTGAATTGGACGTTCAGACACATGTG 420
Db   439 CAACGACTGCTTCCCCGAGTTCATTGTGAATTGGACGTTCAGACACATGTG 498
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   421 TCAGAAAGAAGTGATGAGGACAAAGTGCCGGGGATCAGTCATGTACCATATC 480
Db   499 TCAGAAAGAAGTGATGAGGACAAAGTGCCGGGGATCAGTCATGTACCATATC 558
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   481 AGCGGCCTGTCTCATCCGCCTCCTGTGCCGCCTCCCTCCGGGGAAACTGAA 540
Db   559 AGCGGCCTGTCTCATCCGCCTCCTGTGCCGCCTCCCTCCGGGGAAACTGAA 618
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   541 CTCAGTTTGCATCACGTGCTGCGCAACACCCCTCTTTGTAACGGGCCAAGA 600
Db   619 CTCAGTTTGCATCACGTGCTGCGCAACACCCCTCTTTGTAACGGGCCAAGA 678
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   601 GGGAAGTTCTGCCTCGGGGCTCCGCCACCACCCCGTCCCAAGGCCCAAGAA 660
Db   679 GGGAAGTTCTGCCTCGGGGCTCCGCCACCACCCCGTCCCAAGGCCCAAGAA 738
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   661 AGCCCTCTTCTCCGCCACACTGCTGAGCCTGAAGCCTGAGAGCTCACCGTC 720
Db   739 AGCCCTCTTCTCCGCCACACTGCTGAGCCTGAAGCCTGAGAGCTCACCGTC 798
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   721 TTCCAGCCCTCGCCCCACCCCCACCTCCCTGAGTGAGTGGTTTCTTCCTTT 780
Db   799 TTCCAGCCCTCGCCCCACCCCCACCTCCCTGAGTGAGTGGTTTCTTCCTTT 858
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   781 ATTGCTGGGTGGGGAGGGAGTCCGTGTCTTCTCTTTTGTTCCTGTGCAAAT 840
Db   859 ATTGCTGGGTGGGGAGGGAGTCCGTGTCTTCTCTTTTGTTCCTGTGCAAAT 918
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   841 CTCGGTAAAGCAATTCTGAATAAATTCAGCYTGACYTGATATTTCAGTATTG 900
Db   919 CTCGGTAAAGCAATTCTGAATAAATTCAGCTTGACTGATATTTCAGTATTG 978
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Qy     1 GCCAACTCCGGAGCGTCTGGCGTCGGCGCCCGGGACCGCGGACGGGAGGAGAGACCCG 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   18 GCCAACTCCGGAGGCGGC-GGTGCTTCGGCCCCGGGGAGCGGGAGGGGGAGCAGAGACCCG 76

Qy   61 CAGCGGCGGAGCGAGCCCAGCCGGCGGGATGCAGAGGCTCACCTCGGCTGCCTCTA 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   77 CAGCGGCGGAGCCCCAGCGGCGGGGCCGGATGCAGAGGCTCGCGGGCTCCTCTA 136

Qy 121 AGCTACGACCGTCGTCTCCGCGCGCGCAGCAGCGGGGGCCTCGGCCAGCCACAGC 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 137 AGCTACGACCGTCGTTCCGCGCGCGCGGGGGCCCCAGCAGCAGCCTCGGCCAGCCACAGC 196

Qy 181 CGCTGCAGCCGCGGCAGCGGCTTCGGTGTGCTGTGTGTGCTGCTCCTGATGGGCTTCCG 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 197 CGCTGCAGCCGCGGCAGCGGCTTCGGGGTGCTGTGTGTGCTGCTCCTGATGGGCTTCCG 256

Qy 241 GCCCCGGGGACTCCGGGCGAATGGTGGGGTCCTTAGGCCCATGCGGGCCAACTTTTTGCGGATTGTT 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 257 GCCCCGGGGACTCCGGGCGAATGTGGGTCCTTAGGCCCATGCGGGCCAACTTTTTGCGGATTGTT 316

Qy 301 CTTGCCTCCAGGCCTTTGCGGCTTGCAAATCCAGTGTGTCTACCAGTGTTGAAGAATTCCAGCTGAA 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 317 CTTGCCTCCAGGCCTTTGCGGCTTGCAAATCCAGTGTGTCTACCAGTGTTGAAGAATTCCAGCTGAA 376

Qy 361 CAACGACTGCTTCCTCCCCCGAGTTCATTGTGAATTGCACCGGTCTTGCATCATC 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 377 CAACGACTGCTTCCTCCCCCGAGTTCATTGTGAATTGCACCGGTCTTGCATCATC 436

Qy 421 TCAGAAAGAAGTGATTGAGCAAAGTGCCGGGGATCATGTACCGGCAAGTCCTGTGCATCATC 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 437 TCAGAAAGAAGTGATTGAGCAAAGTGCCGGGGATCATGTACCGGCAAGTCCTGTGCATCATC 496

Qy 481 AGCGGCGCTGTCTCATCGCGTCCTGCGGGTACCAGTCCTTTGTCTCCCCAGGGAAAACTGAA 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 497 AGCGGCGCTGTCTCATCGCGTCCTGCGGGTACCAGTCCTTTGTCTCCCCAGGGAAAACTGAA 556

Qy 541 CTTCAGTTTGCATCAGCTGCTGCAACACCCCTCTCTTTGTAACGGCCAAGGCCCAAGAAAAG 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 557 CTTCAGTTTGCATCAGCTGCTGCAACACCCCTCTCTTTGTAACGGCCAAGGCCCAAGAAAAG 616

Qy 601 GGGAAGTTCTGCCTCGGCCCTCGGCCGGCGTCCCGCCACCATCCTGTTCCTCAAATT 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 617 GGGAAGTTCTGCCTCGGCCCTCGGCCGGCGTCCCGCCACCATCCTGTTCCTCAAATT 676

Qy 661 AGCCCTCTTCTCGCGACACTGCTGCTGAGCGTGAAGGAGAGATGCCACCCCTCCTGCATTGTTC 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 677 AGCCCTCTTCTCGCGACACTGCTGAACTGAAGGAGAGATGCCACCCCTCCTGCATTGTTC 736

Qy 721 TTCCAGCCCTCGGCCCCCCAACCCCCTCCCAACTCCCTGAGTGGAGTTTCTTCTGGGGTGTCCTTTTT 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 737 TTCCAGCCCTCGGCCCCCCAACCCCCTCCCAACTCCCTGAGTGGAGTTTCTTCTGGGGTGTCCTTTTT 796

Qy 781 ATTCTGGGTAGGGAGCGGGAGCGTCCGGTTGTCTTCTCTGTTGTTCCTGTGCAAAATAATGAAAGAG 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 797 ATTCTGGGTAGGGAGCGGGAGCGTCCGGTTGTCTTCTCTGTTGTTCCTGTGCAAAATAATGAAAGGA 856

Qy 841 CTCGGGTAAAGCANTTCTGAATAAAATTCAGCYTGACTGAATTTCAGTATGTACTTGAAGGA 900
         ||||||||||||| | ||||||||||||||||||||:||||||||||||||||||
Db 857 CTCGGTAAAGCANTTCTGAATAAAATTCAGCTTGACTGAATTTCAGTATGTACTTGAAGGA 916

Qy 901 AGGAGGTGGAGTGAAAGTTCACCCCCATNGTCTGTGTAACCGGAGTCAAGGCCAGGCTGGC 960
         ||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db 917 AGGAGGTGGAGTGAAAGTTCACCCCCATGTCTGTGTAACCGGAGTCAAGGCCAGGCTGGC 976

Qy 961 AGAGTCNGTCCTTAGAAGTCACTGAGTGGCCATCGCCTTTTGTAAAGCCTCCAGTGTC 1020
         ||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db 977 AGAGTCAGTCCTTAGAAGTCACTGAGTGGCCATCGCCTTTTGTAAAGCCTCCAGTGTC 1036

Qy 1021 CANTTCCATCCCTGATNGGGGGCANTAGTTTGAGACTGAGAGTGAGAGTGACGTTTTCTTAG 1080
         |||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db 1037 CATTTCCATCCCTGATGGGGGCANTAGTTTGAGACTGAGAGTGAGAGTGACGTTTTCTTAG 1096

Qy 1081 GGCTGGAGGGCCAGTTCCCACTCAAAGGCTCTCCTCT 1140
         |||||||||||||||||||||||||||||||||||||
Db 1097 GGCTGAGGGGCCAGTTCCCACTCAAAGGCTCTCCTCT 1156

Qy 1141 GAAACCANTTCTCTGCAGCACAGAATTGGCTGGTTTCGGCCGCCTGGTTGGGCTTAGTGACT 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1157 GAAACCANTTCTCTGCAGCACAGAATTGGCTGGTTTCGGCCGCCTGAGTTGGGCTTAGTGACT 1216

Qy 1201 CGAGACTCAATGACTAGGACTTAGACTGGGCTGGGGGCTCGGCCGCCTCTGAAAAGTTGCTTAAGA 1260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1217 CGAGACTCAATGACTAGGACTTAGACTGGGCTGGGGGCTCGCCTTCTGAAAAGTTGCTTAAGA 1276

Qy 1261 AAATCTTTCTCACGTTCTCCTTGCAGAGACTGCGCGGGCGGGAAGAGCAACGGGGGCCT 1320
         |||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db 1277 AAATCTTTCTCAGTTCTCCTTGCAGAGACTGCGCGGGCGGGAAGAGCAACGGGGGCCT 1336

Qy 1321 GCACAAAAGCGGCGCGTCGGGTCGGTGGCCATGGCCAGCGCCGGCGCCTTCTTCGGTGGT 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1337 GCACAAAGCGGCGCGTCGGGTCGGTGGCCATGGCCAGCGCCGGCGCCTTCTTCGGTGGT 1396

Qy 1381 TGGCGTGCTGCAGCGACCAGGCGACACAGCAGCACCTGCACGCACAGGGACCACTGAA 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1397 TGGCGTGCTGCAGCGACCAGGCGACACAGCAGCACCTGCACGCACAGGGACCACTGAA 1456

Qy 1441 GCGAGGACAACCGTGTACAGGAGCGGGGGTTGATGACCGAGACTGAGGTAGAAAACGTCTCCG 1500
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1457 GCGAGGACAACCGTGTACAGGAGCGGGGGTTGATGACCGAGACTGAGGTAGAAAACGTCTCCG 1516

Qy 1501 AGAAGGGGAGGAGGGATCANTGTACGGGCCCCGGGAAGTAGGACCTCGTCCAGTGCTGCTGGGTT 1560
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1517 AGAAGGGGAGGAGGGATCANTGTACGGGCCCCGGGAAGTAGGACCTCGTCCAGTGCTGCTGGGGT 1576

Qy 1561 TGGCCGCAGCCATGATCTCCGAATCTCGGTTGGGCATCCNAGCATACGGCCCAAGTCACAA 1620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1577 TGGCCGCAGCCATGATCCTCCGAATCTCGGTTGGGCATCCCAGCATACGGTCNTCACAA 1636

Qy 1621 CAATCAGCCCTGGGCAGACACGAGCGAGCAGGAGGGAGAGAAAAGAAAAACAGCAT 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1637 CAATCAGCGCCTGGGCAGACACGAGCGAGCAGGAGGGAGAGAAAAGAAAAACAGCAT 1696

Qy 1681 GAGAACACAGTAAATGAATAAAAAACCATAAAATATTAGCCCCTCTTGTTCGTTACTG 1740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1697 GAGAACACAGTAAATAAATAAAAAACCATAAAATATTAGCCCCTCTTGTTCGTTACTG 1756

Qy 1741 GCCAGGAAATGGTACCAANTTTCAGTGTTGACTTGACAGCTTTGCCACAAGCAA 1800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1757 GCCAGGAAATGGTACCAANTTTTCAGTGTTGACTTGACAGCTTTGCCACAAGCAA 1816

Qy 1801 GAGAGAAATTTAACACTGTTTTCAAACCCGGGGGAGTTGGCGTGTTAAAGAAAGACCATTA 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1817 GAGAGAAATTTAACACTGTTTTCAAACCCGGGGGAGTTGGCGTGTTAAAGAAAGACCATTA 1876

Qy 1861 AATGCTTTAGACAGTGTAAAAAAAAAAAA 1887
         ||||||||||||||||||||||||| |
Db 1877 AATGCTTTAGACAGTGTAAAAAAAAACA 1903

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; PRIOR APPLICATION NUMBER: US 60/126,906
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/132,099
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5775
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4454
; LENGTH: 1918
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-808-383-4454

Query Match        98.5%;       Score 1869.4;   DB 31;    Length 1918;
Best Local Similarity   99.7%;    Pred. No. 0;   Mismatches    3;   Indels    1;   Gaps    1;
Matches 1881;   Conservative    2;   Mismatches    3;   Indels    1;   Gaps    1;

Qy      1  GCCAAACTCCGGAGCGCTCTGGTGCTCGGCCGCCCGGGGAGCGGACGAGAGACCCG   60
           ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db     18  GCCAACTCCGGAGCGGC-GGTGCTCGGCCCGGGGAGCGGACGGGGAGGAGAGACCCG   76

Qy     61  CAGCCCGGGAGCGCCCAGCGAGCGGGGGGGGGCGGGCACGGGGCACCTCGGCTCCTCTA  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     77  CAGCCCGGGAGCCCGGGCGAGCGGGGGCGCACCTGCGGCTCCTCTA  136

Qy    121  AGCTACGACCTGTTCGCTCTCCCGCGGCAGCAGCCGCTCGGCGAGCCACAGC  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    137  AGCTACGACCGTGTCTCTCCGCGGCAGCAGCAGCCGCTCGGCGAGCCACAGC  196

Qy    181  CGCTGCAGCCGCCGGGCCAGCCTCGCGTGCTGTCGCCTCCTCTGAGTGCCCTCTCCCG  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    197  CGCTGCAGCCGGGGGCAGCCTCGCGTGCTGTCGCCTCCTCTGAGTGCCCTCTCCCG  256

Qy    241  GCCCCGGGACTCCGGGAGAAATGTGGGTCCTAGGCATCGCGCGCAACTTTTTTGCGGATTGTT  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    257  GCCCCGGGGACTCCGGGAGAAATGTGGGTCCTAGGCATCGCGCGCAACTTTTTTGCGGATTGTT  316

Qy    301  CTTGCTTCCAGGCTTTGCCGCTGCAAAATCCAGTCAGTGCTACCAGTTCCAGCTGAA  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    317  CTTGCTTCCAGGCTTTGCCGCTGCAAAATCCAGTCAGTGTACCAGTGTGAAGAAATTCCAGCTGAA  376

Qy    361  CAACGACTGCTCCTCCCCGAGTTCATTGTGGAATTGCACGGTGAAGGTTCAAGACATGTG  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    377  CAACGACTCTCCTCCCCGAGTTCATTGTGAATTGCACGGTGAAGGTTCAAGACATGTG  436

Qy    421  TCAGAAAAGAAGTGATGGACAAAGTGCCGGGATCAAGTTCCTGCCATCATC  480
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db    437  TCAGAAAAGAAGTGATGGAGCAAAGTCCCGGGATCAATGTACCGCAAGTCCTGTGCATCATC  496

Qy    481  AGGGGCCTGTCTCATCGGCTCTGCCGGGTACCAGTCCTCTCTGCTCCCCAGGGAAACTGAA  540
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db    497  AGCGGCCTGTCTCATCGGCTCTGCGGGGTACCAGTCCTCTTCGCTCCCCAGGGAAACTGAA  556

Qy    541  CTCAGTTTGCATCAGCTGCTGCAACACCCCTCTCTTTGTAACGGGCCCAAGAGAAAG  600
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db    557  CTCAGTTTGCATCAGCTGCTGCAACACCCCTCTCTTTGTAACGGGCCCAAGAGAAAAG  616

Qy    601  GGGAAGTTCTGCCTCGGCCCTCAGGCCACAGGGCTCCGCCACCACCACCATCCTCAAAATT  660
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db    617  GGGAAGTTCTGCCTCGGCCCTCAGGCCACAGGGCTCCGCCACCACCATCCTGTTCCTCAAAAT  676

Qy    661  AGCCCTCTTCTCGGCACACTGCCTCGGCCCTCAGGCCACAGGGCTCCGCCACCATCCTGTTCCTCAATTGTTC  720
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db    677  AGCCCTCTTCTCGGCACACTGCCTCGGCCCTCAGGCTCCGCCACCATCCTGTTCCTCAATTGTTC  736

Qy    721  TTCCCAGCGCCCTCGCCCCCAACCCCACCTCCCGAGTGAGTTCTTCTTCTGGGTGTCCTTTT  780
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db    737  TTCCAGCGCCTCGCCCCCAACCCCCACCTCCCGAGTGAGTTCTTCTTCTGGGTGTCCTTTT  796

Qy    781  ATTCTGGGTAGGGAGCGGGGAGTCCGGTGTTCTCTTTTTGTTCCTGTGCCAAATAAATGAAAGAG  840
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db    797  ATTCTGGGTAGGGAGCGGGGAGTCCGGTGTTCTCTTTTGTTCCTGTGCCAAATAAATGAAAGAG  856

Qy    841  CTCGGTAAAGCATTCTGAATAAATTCAGCYTGACTGAATTTTCAGTATATGTACTTGAAGGA  900
           ||||||||||||||||||||||||||||||||||||||||||||||||

Db    857  CTCGGTAAAGCATTCTGAATAAATTCAGCTTGACTGAATTTTCAGTATGTACTTGAAGGA  916

Qy    901  AGGAGGTGGAGTGGAAAGTTCACCCCCATGTCTGGTAACCTTCAGGCCAGGCTGGC  960
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db    917  AGGAGGTGGAGTGGAAAGTTCACCCCCATGTCTGTAACCTTCAGGCCAGGCTGGC  976

Qy    961  AGAGTCWGTCCCTTAGAAGTCACTGAGGTGGGCATCTGCCTTTTGTGTAAAACCTCCAGTGTC  1020
           |||||||:|||||||||||||||||||||||||||||||||||||||||||:|||||||
Db    977  AGAGTCAGTCCCTTAGAAGTCACTGAGGTGGGCATCTGCCTTTTGTGTAAAACCTCCAGTGTC  1036

Qy   1021  CATTCCATCCCTGATGGGGGCATAGTTGTTGGACTGCAGGTGCAGGTGAGAGTGAGAGTGACGTTTTCTTAG  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1037  CATTCCATCCCTGATGGGGGGCATAGTTGTTGGACTGCAGGTGCAGGTGAGAGTGAGAGTGACGTTTTCTTAG  1096

Qy   1081  GGCTGGAGGGGCCAGTTCCCACTCAGGCCTCCCTCGGCTTGACATTCAAACTTCATGCTCCT  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1097  GGCTGGAGGGGCCAGTTCCCACTCAGGCCTCCCTCGGCTTGACATTCAAACTTCATGCTCCT  1156

Qy   1141  GAAAACCATTCTCTGCAGCAGAGAATTGGCTGGGTTCGGCCCTGAGTTGGGCCTGAGTTGACT  1200
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1157  GAAAACCATTCTCTGCAGCAGAGAATTGGCTGGGTTCGGCCCTGAGTTGGGCCTGAGTTGACT  1216

Qy   1201  CGAGACTCAATGACTGGGACTTAGACTGGGGGCTTCGGCGCTCGCGCTCTGAAAAGTCGTTCTTAAGA  1260
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1217  CGAGACTCAAATGACTGGGACTTAGACTGGGGGCTTCGGCGCTCGCGCTCTGAAAAGTCGTTCTTAAGA  1276

Qy   1261  AAATCTTCTCAGTTCTCTCCTTCGCAGAGACGAGACTGGGGCTCTGACATTGCAGACTCATTCATGCTCCG  1320
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1277  AAATCTTCTCAGTTCTCTCCTTCGCAGAGACTGGGGCTCTGACATTGCAGACTGCAGAGGTCATTCATGCTCCG  1336

Qy   1321  GCACAAAAGCGGGGGCGCTGTCGGTGGGGAGTGCGGCGCCATGTACGGCGGCGGCGGCTTCTCGGGGT  1380
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1337  GCACAAAAGCGGGGGCGCTGTCGGTGGGGAGTGCGGCGCCATGTACGGCGGCGGCGGCTTCTCGTGGT  1396

Qy   1381  TGGCGTGCTGCAGCGACGACGAGGAGGCGGGTTGATAGACCGAGGTAGAAAACGTCTCCG  1440
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1397  TGGCGTGCTGCAGCGACGACGAGGAGGCGGGTTGATAGACCGAGGTAGAAAACGTCTCCG  1456

Qy   1441  GCGAGGACACCGTGTACAGGAGGAGCCGGGTTGATAGACCGAGGTAGAAAACGTCTCTGCTCT  1500
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1457  GCGAGGACACCGTGTACAGGAGGAGCCGGGTTGATAGACCGAGGTAGAAAACGTCTCG  1516

Qy   1501  AGAAGGGGAGGAGGATCATGTACGCCCGGAAGTAGGACTCGTCCAGTCGTGCTGGGGTT  1560
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1517  AGAAGGGGAGGAGGATCATGTACGCCCGGAAGTAGGACTCGTCCAGTCGTGCTGGGGTT  1576

Qy   1561  TGGCCGCCAGCCATGATCCTCCGGAATCGTGGTTGGGCATCCAGCATACGGCCAATGTCACAA  1620
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1577  TGGCCGCCAGCCATGATCCTCCGGAATCGTGGTTGGGCATCCAGCATACGGCCAATGTCACAA  1636

Qy   1621  CAATCAGCCCTGGGGAGACAGGAGGAGGAGAGAGAAAAACACAGCAT  1680
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1637  CAATCAGCCCTGGGGAGACAGGAGGAGGAGGAGAGAGAAAAACACAGCAT  1696

Qy   1681  GAGAGACACAGTAAATGAATAAAACCATAAAAATATTTAGCCCCTCTGTTTGTGTCTTACTG  1740
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1697  GAGAACACAGTAAATAAATAAAACCATAAAAATATTTAGCCCCTCTGTTTTTGTGTCTTACTG  1756

Qy   1741  GCCAGGAAATGGTACCAATTTTTCAGTGTTGGACTTGACAGCTTCTTTTGCCACAAGCAA  1800
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1757  GCCAGGAAATGGTACCAATTTTTCAGTGTTGGACTTGACAGCTTCTTTTGCCACAAGCAA  1816

Qy   1801  GAGAGAATTTAACACTGTTTCAAAACCCGGGGGGAGTTGGCTGTGTTAAAGAAGACCATTA  1860
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1817  GAGAGAATTTAACACTGTTTCAAAACCCGGGGGGAGTTGGCTGTGTTAAAGAAGACCATTA  1876

Qy   1861  AATGCTTTAGACAGTGTAAAAAAAAAA  1887
           ||||||||||||||||||| |
Db   1877  AATGCTTTAGACAGTGTAAAAAAAAACA  1903
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RESULT 8

US-09-652-121-7293/c
; Sequence 7293, Application US/09652121
; GENERAL INFORMATION:
; APPLICANT: Distefano, Peter
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1188-001
; CURRENT APPLICATION NUMBER: US/09/652,121
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,129
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 7615
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7293
; LENGTH: 1925
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-652-121-7293

Query Match   98.2%;   Score 1863.2;   DB 25;   Length 1925;
Best Local Similarity   99.6%;   Pred. No. 0;
Matches 1876;   Conservative   2;   Mismatches   5;   Indels   1;   Gaps   1;

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Qy      1 GCCAACTCCGGAGGCTCTGGTWGTCTCGGCCCGGAGCCGAGCGAGGAGCAGAGAGACCCG 60
          ||||||||||||||| ||||| |||||||||||||||||||||||||||||||||||||
Db   1905 GCCAACTCCGGAGGCGC--GGTGCTCGGCCCGGAGCCGAGCGAGGAGCAGAGAGACCCG 1847

Qy     61 CAGCCCGGGAGCCGACGCGGCGGGATGCAGGCGCACCTGCGGCTCTCTA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1846 CAGCCCGGGAGCCGACGCGGCGGGATGCAGGCGCACCTGCGGCTCTCTA 1787

Qy    121 AGCTACGACCCGTCGTCCGGGCCGCACCAGCAGCCCGAGCAGC 180
          |||||||||||||||||||||||||||||||||||||||||||
Db   1786 AGCTACGACCCGTCGTCCGGGCACCAGCAGCCCGAGCCAGC 1727

Qy    181 CGCTGCAGCCGGGCGCAGCCTCCGGCTGCTGCCCTCCCG 240
          |||||||||||||||||||||||||||||||||||||||
Db   1726 CGCTGCAGCCGGGCGCAGCCTCCGGCTGCTGCCCTCTCCG 1667

Qy    241 GCCCCGGGGACTCCGGAGAAATGTGGGTCCTAGGCACCG 300
          |||||||||||||||||||||||||||||||||||||||
Db   1666 GCCCCGGGGACTCCGGAGAAATGTGGGTCCTAGGCACCG 1607

Qy    301 CTTGCTTCCAGCCTTTGCGCTGCAAATCCAGTGCCAGTG 360
          |||||||||||||||||||||||||||||||||||||||
Db   1606 CTTGCTTCCAGCCTTTGCGCTGCAAATCCAGTGCCAGTG 1547

Qy    361 CAACGACTGCTCTCCCCGGAGTTCATTGTGAAATTCAAG 420
          |||||||||||||||||||||||||||||||||||||||
Db   1546 CAACGACTGCTCTCCCCGAGTTCATTGTGAAATTCAAG 1487

Qy    421 TCAGAAAGAAGTGATGGAGCAAAGTGCCGGGAATCATGT 480
          |||||||||||||||||||||||||||||||||||||||
Db   1486 TCAGAAAGAAGTGATGGAGCAAAGTGCCGGGAATCATGT 1427

Qy    481 AGCGGCCTGTCTCATCGGCCTCTGCCGGGTACCAGTCCT 540
          |||||||||||||||||||||||||||||||||||||||
Db   1426 AGCGGCCTGTCTCATCGGCCTCTGCCGGGTACCAGTCCT 1367

Qy    541 CTCAGTTTGCATCAGCTGCTCAACACACCCTCTTTGTTA 600
          |||||||||||||||||||||||||||||||||||||||
Db   1366 CTCAGTTTGCATCAGCTGCTCAACACACCCTCTTTGTTA 1307

Qy    601 GGGAAGTTCTGCCTCGGCCCTCAGGCGTCCGGCCAGGGC 660
          |||||||||||||||||||||||||||||||||||||||
Db   1306 GGGAAGTTCTGCCTCGGCCCTCAGGCGTCCGGCCAGGGC 1247

Qy    661 AGCCCTCTTCTCTGGCACACTGTGAAGCTGAGAGAGATG 720
          |||||||||||||||||||||||||||||||||||||||
Db   1246 AGCCCTCTTCTCTGGCACACTGTGAAGCTGAGAGAGATG 1187

Qy    721 TTCCAGCGCCTCGCCCCCCAACCCCACCTCCCTGAGTGA 780
          |||||||||||||||||||||||||||||||||||||||
Db   1186 TTCCAGCGCCTCGCCCCCCAACCCCACCTCCCTGAGTGA 1127
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```
RESULT 9

US-09-652-128-9375/c

Db      46  AATGCTTTAGACAGTGTATTTAAA 23

Qy    1861  AATGCTTTAGACAGTGTAAAAAAA 1884
            |||||||||||||||||| |||| |||

Sequence 9375, Application US/09652128

GENERAL INFORMATION:
APPLICANT:
APPLICANT:  Shyjan, Andrew W.
APPLICANT:  Holtzman, Douglas A.
TITLE OF INVENTION:  NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION:  THEREFOR
FILE REFERENCE:  1600.1171-001
CURRENT APPLICATION NUMBER:  US/09/652,128
CURRENT FILING DATE:  2000-08-30
PRIOR APPLICATION NUMBER:  60/151,133
PRIOR FILING DATE:  1999-08-30
NUMBER OF SEQ ID NOS:  10265
SOFTWARE:  FastSEQ for Windows Version 4.0
SEQ ID NO 9375
  LENGTH:  1925
  TYPE:  DNA
  ORGANISM:  Homo sapiens
US-09-652-128-9375

Query Match             98.2%;  Score 1863.2;  DB 25;  Length 1925;
Best Local Similarity   99.6%;  Pred. No.  0;
Matches 1876;  Conservative  2;  Mismatches  5;  Indels  1;  Gaps  1;
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Qy     1  GCCAACTCCGGAGGCTCTGTGCTCGGCCCGCGAGGCGGCGGGAGGCAGAGACCCG 60
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db  1905  GCCAACTCCGGAGGCGGC-GGTGCTCGGCCCGGGGAGGCGGCGGGAGGCAGAGACCCG 1847

Qy    61  CAGCCGGGAGGCCCGAGCCCGGGGGATGGAGGGTCTCCGGGCACCTCGGGCTCCTCTA 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1846  CAGCCGGGAGGCCCGAGCCCGGGGGATGGAGGGTCTCCGGGCACCTCGGGCTCCTCTA 1787

Qy   121  AGCTACGACCGTCGTCTCCGGCGCGCGCGCGCGCGCCACGCACAGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||
Db  1786  AGCTACGACCGTCGTCTCCGGCGCGCGCGCGCGCGCCACGCACAGC 1727

Qy   181  CGCTGCAGCGCGGGGGCAGCCTCCGCGTCGTCGCCTGCCCTCTGCCCTCTCCCG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1726  CGCTGCAGCGCGGGGGCAGCCTCCGCGTCGTCGCCTGCCCTCTGCCCTCTCCCG 1667

Qy   241  GCCCCGGGACTCCGGAGAAATGTGGGGTCCTCCGGGCCATCGCGGGCCAACTTTTTTGCGGATTGTT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1666  GCCCCGGGACTCCGGAGAAATGTGGGGTCCTCCGGGCCATCGCGGGCCAACTTTTTTGCGGATTGTT 1607

Qy   301  CTTGCTTCCAGCGCTTTCGCTCGCAAATCCCAGTGTGAAGAAATTCCAGCTGAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1606  CTTGCTTCCAGCGCTTTCGCTCGCAAATCCCAGTGTGAAGAAATTCCAGCTGAA 1547

Qy   361  CAACGACTGCTCCTCCCCGAGTTCATTGTGAATTGCACGGTTCAAGACATGTG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1546  CAACGACTGCTCCTCCCCGAGTTCATTGTGAATTGCACGGTTCAAGACATGTG 1487

Qy   421  TCAGAAAGAAGTGATGGAGCAAAGTGCCGGGATCATGTACCGCAAGTCTCGTGTGCATCATC 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1486  TCAGAAAGAAGTGATGGAGCAAAGTGCCGGGATCATGTACCGCAAGTCTCGTGTGCATCATC 1427

Qy   481  AGCGGCCTGTGTCTCATCCCCTCTGCCGGTACCAGTCCTTCTCTGCTCCCCAGGGAAACTGAA 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1426  AGCGGCCTGTGTCTCATCCCCTCTGCCGGTACCAGTCCTTCTCTGCTCCCCAGGGAAACTGAA 1367

Qy   541  CTCAGTTTGCATCAGCTGCTGCAACACCCCTCTTTGTAACGGGGGGCCAAGAAAAG 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1366  CTCAGTTTGCATCAGCTGCTGCAACACCCCTCTTTGTAACGGGGCCAAGAAAAG 1307

Qy   601  GGGAAGTTCTGCCTCGGCCCTCCGCACCACCATCCGTGTTCCTCAAATT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1306  GGGAAGTTCTGCCTCGGCCCTCCGCACCACCATCCGTGTTCCTCAAATT 1247
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Db  1306  GGGAAGTTCTGCCTCGGCCCTCCGCACCACCATCCGTGTTCCTCAAATT 1247

Qy   661  AGCCCTCTTCTCTGCAACACTCGTGCAGCTGAAGCGATGGCCACCCGCGATTGTTC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1246  AGCCCTCTTCTCTGGCAACACTGCTGAAGCGATGGCCACCCGCGATTGTTC 1187

Qy   721  TTCCAGCCCTCTGCGCCCCCAACCCCCACCCTCCCTGAGTGGAGTTTCTCTGGGTT 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1186  TTCCAGCCCTCTGGCCCCCAACCCCCACCCTCCCTGAGTGGAGTTTCTCTGGGTT 1127

Qy   781  ATTCTGGGTAGGGAGGGGGAGTCCGTGTTCTGTTCTCTGTTTTGCAAATAATGAAAAGAG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1126  ATTCTGGGTAGGGAGGGGGAGTCCGTGTTCTGTTCTCTGTTTTGCAAATAATGAAAAGAG 1067

Qy   841  CTCGGTAAAGCATTCTGAATAAATTCAGCYTGACTGAATTTCAGTAYGTACTTGAAGGA 900
          |||||||||||||||||||||||||||||:||||||||||||||||:|||||||||||||
Db  1066  CTCGGTAAAGCATTCTGAATAAATTCAGCTTGACTGAATTTCAGTATGTACTTGAAGGA 1007

Qy   901  AGGAGGTGGAGTGAAAGTTCACCCCATGTCTGTGTAACCGGAGTCAAGGCCGCTGGC 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1006  AGGAGGTGGAGTGAAAGTTCACCCCATGTCTGTGTAACCGGAGTCAAGGCCGCTGGC 947

Qy   961  AGAGTCWGTCCTTAGAAAGTCACTGAGGTGGGCCATCCGCCTTTTGTAAAGCCCCAGTGTC 1020
          ||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   946  AGAGTCAGTCCTTAGAAAGTCACTGAGGTGGGCCATCCGCCTTTTGTAAAGCCCCAGTGTC 887

Qy  1021  CATTCCATCCCTGATGGGGGGCCATAGTTGTTGAGACTGCAGAGTGAGAGTGACGTTTTCTTAG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   886  CATTCCATCCCTGATGGGGGGCCATAGTTGTTGAGACTGCAGAGTGAGAGTGACGTTTTCTTAG 827

Qy  1081  GGCTGGGAGGGCCAGTTCCCACTCACGGCTCCCTCCGCTTGAGACTGCAGAGTGAGTTTGGCTCT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   826  GGCTGGGAGGGCCAGTTCCCACTCACGGCTCCCTCCGCTTGAGACTGCAGAGTGAGTTTGGCTCT 767

Qy  1141  GAAAACCAATTCTCTGCCACGAGAAATGGCTGTGGTTTTCGGCTGGGTGGGGTCTCTAGTGACT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   766  GAAAACCAATTCTCTGCCACGAGAAATGGCTGTGGTTTTCGGCTGGGTGGGGTCTCTAGTGACT 707

Qy  1201  CGAGACTCAATGACTGGGGACTTAGACTGTGGGGCTCGGCGCCTTCGGCTCTGGAAAAGTGCTTAAGA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   706  CGAGACTCAATGACTGGGGACTTAGACTGTGGGGCTCGGCGCCTTCGGCTCTGGAAAAGTGCTTAAGA 647

Qy  1261  AAATCTTCTCAGTTCTCCTTGCAGAGGAGACTGGGCGCGCGGGAGGCGGAGAGCAACGGCGCGCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   646  AAATCTTCTCAGTTCTCCTTGCAGAGGAGACTGGGCGCGCGGGAGGCGGAGAGCAACGGCGCGCT 587

Qy  1321  GCACAAAAGCGGCGCTTGTCGGTGGTGGGAGTCGCAGTGTACCGCGACAGGGCGCTTCTCGTGGT 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   586  GCACAAAAGCGGCGCCTGTCGGTGGTGGGAGTCGCAGTGTACCGCGACAGGGCGCTTCTCGTGGT 527

Qy  1381  TGGCGTGCTGCAGCGACAGCGGCCAGCACACCAGCACCCGCGCGGAAACTGCT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   526  TGGCGTGCTGCAGCGACAGCGGCCAGCACACCAGCACCCGCGCGGAAACTGCT 467

Qy  1441  GCGAGGACACCGTGTACAGGAGCGGGGTTGATGACCGAGGTGAGAAAACGTCTCCG 1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   466  GCGAGGACACCGTGTACAGGAGCGGGGTTGATGACCGAGGTGAGAAAACGTCTCCG 407

Qy  1501  AGAAGGGGAGGAGGGGATCATGTACGGCCGGAAGTAGGACCTCGCTGCTTGGGTT 1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   406  AGAAGGGGAGGAGGGGATCATGTACGGCCGGAAGTAGGACCTCGCTGCTTGGGTT 347

Qy  1561  TGGCCGCAGCCATGAATCCTCCGAATCGGTTGGGCATCCAGCATAGGGCCAATGTCACAA 1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   346  TGGCCGCAGCCATGAATCCTCCGAATCGGTTGGGCATCCAGCATAGGGCCAATGTCACAA 287

Qy  1621  CAATCAGCGCCCTGGGCAGACAGCAGGAGAGACAGAGAAAGAGAGAAAACAGAGCAT 1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   286  CAATCAGCGCCCTGGGCAGACAGCAGGAGAGACAGAGAAAGAGAGAAAACAGAGCAT 227

Qy  1681  GAGAACACAGTAAAATAAAAACCATAAAAATATTAGCCCCTCTGTTCTTCGTGTGCTTACTG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   226  GAGAACACAGTAAAATAAAAACCATAAAAATATTAGCCCCTCTGTTCTTCGTGTGCTTACTG 167
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RESULT 10
US-09-652-917-3346/c
Sequence 3346, Application US/09652917
GENERAL INFORMATION:
    APPLICANT: Shyjan, Andrew W.
    APPLICANT: Holtzman, Douglas A.
    APPLICANT: DiStefano, Peter
    TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
    TITLE OF INVENTION: THEREFOR
    FILE REFERENCE: 1600.1170-001
    CURRENT APPLICATION NUMBER: US/09/652,917
    CURRENT FILING DATE: 2000-08-30
    PRIOR APPLICATION NUMBER: 60/151,422
    PRIOR FILING DATE: 1999-08-30
    NUMBER OF SEQ ID NOS: 3855
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 3346
    LENGTH: 1925
    TYPE: DNA
    ORGANISM: Homo sapiens
US-09-652-917-3346

    Query Match     98.2%;  Score 1863.2;  DB 25;  Length 1925;
    Best Local Similarity   99.6%;  Pred. No. 0;
    Matches 1876;  Conservative 2;  Mismatches  5;  Indels  1;  Gaps  1;
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Qy 1 GCCAACTCCGGAGGCGCTCTGGTTGCTCGCGCCGCCGGAGGCGACGGGAGGGAGAGACCCG 60
       ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db 1905 GCCAACTCCGGAGGCGGC-GGTGCTCGCGCCGCCGGGAGGCGACGGGAGGGAGAGACCCG 1847

Qy 61 CAGCCGGGGAGCCCGAGCGCGGCGGGATGCAGGCTCCGGAGCCGGCCGGGGCTCCTCTA 120
        ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1846 CAGCCGGGGAGCCCGACCGCGGCGGGATGCAGGCTCCGGAGCCGGCCGGGGCTCCTCTA 1787

Qy 121 AGCTACGGACCGTTCGTCTCTCCGGGGCAGCAGCCGGGGGGGGCCCAGCCGGCCACAGC 180
        |||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db 1786 AGCTACGAACCGTTCGTCTCTCCGGGGCAGCAGCCGGGGGGGGCCCAGCCGGCCACAGC 1727

Qy 181 CGCTGCAGCCGCGGGCAGCCTCCGCTGCTGTGCCGCTGCCCTCTCCCG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db 1726 CGCTGCAGCCGCGGGCAGCCTCCGCTGCTGTGCCGCTGCCCTCTCCCG 1667

Qy 241 GCCCCGGGACTCCGGGAGAATGTGGGGTCCTAGGCATCGGGCCAACTTTTTCGGGATTGTT 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1666 GCCCCGGGACTCCGGGAGAATGTGGGGTCCTAGGCATCGGGCCAACTTTTTCGGGATTGTT 1607

Qy 301 CTTGCTTCCAGGCTTTGCGCTGCAGTCGTAGGAATTCCAGCTGAA 360
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Db 1606 CTTGCTTCCAGGCTTTGCGCTGCAGTCGTAGGAATTCCAGCTGAA 1547

Qy 361 CAACGACTGCTCCTCCCCGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACACATGTG 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1546 CAACGACTGCTCCTCCCCGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACACATGTG 1487

Qy 421 TCAGAAAGAAGTGATGGAGCAAAGTGCCGGGATCATGTACCGCAAGTCCTTGTGCATCATC 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1486 TCAGAAAGAAGTGATGGAGCAAAGTGCCGGGATCATGTACCGCAAGTCCTTGTGCATCATC 1427

Qy 481 AGCGGGCCTGTCTCATCGCCTCTTGCTCTCCCAGGGAGAAACTGAA 540
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Db 1426 AGCGGGCCTGTCTCATCGCCTCTTGCTCTCCCAGGGAGAAACTGAA 1367

Qy 541 CTCAGTTTGCATCAGTGTCTGCAAACACCCCTCTTTGTAACGGCCAAGGCCCAAGAAAAG 600
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1366 CTCAGTTTGCATCAGTGTCTGCAAACACCCCTCTTTGTAACGGCCAAGGCCCAAGAAAAG 1307

Qy 601 GGGAAGTTCTGCCTCTCGCCGCCTCCAGGCCTCAGGGCCTCCGGCCACCAGGCCCAAATT 660
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Db 1306 GGGAAGTTCTGCCTCTCGCCGCCTCCAGGCCTCAGGGCCTCCGGCCACCAGGCCCAAATT 1247

Qy 661 AGCCCTCTTCTCGGGCACACTGTGAAGCTGAAGGAGATGCCACCCCCTCCCTCGGTTGTTC 720
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Db 1246 AGCCCTCTTCTCGGGCACACTGTGAAGCTGAAGGAGATGCCACCCCCTCCCTCGGTTGTTC 1187

Qy 721 TTCCAGCCCTCGCCCCCAACCCCACCTCCCTGAGTGGAGTTTCTTGGGGTGTCCCTTTT 780
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Db 1186 TTCCAGCCCTCGCCCCCAACCCCACCTCCCTGAGTGGAGTTTCTTGGGGTGTCCCTTTT 1127

Qy 781 ATTCTCGGGTAGGGAGCGGGAGTCCGTGTTCTCTTTTTTGTTCCTTGTGCAAATAATGAAAAGAG 840
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Db 1126 ATTCTCGGGTAGGGAGCGGGAGTCCGTGTTCTCTTTTTTGTTCCTTGTGCAAATAATGAAAAGAG 1067

Qy 841 CTCGGTAAAGCATTCTGAATAAATTCAGCYTGACTGAATTTTCAGTATGTTACTTTGAGGA 900
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Db 1066 CTCGGTAAAGCATTCTGAATAAATTCAGCTTGACTGAATTTTCAGTATGTTACTTTGAAGA 1007

Qy 901 AGGAGGTGGAGTGAAAGTTCACCCCCCATGTCTCGTGTAACCGGAGTCAAGGCCAGGCTGC 960
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Db 1006 AGGAGGTGGAGTGAAAGTTCACCCCCCATGTCTCGTGTAACCGGAGTCAAGGCCAGGCTGC 947

Qy 961 AGAGTCWGTCCTTAGAAGTCACTGAGGGTGGGCAATCTGCCTTTTGTTAAAGCCTCCAGTGTC 1020
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Db 946 AGAGTCAGTCCTTAGAAGTCACTGAGGGTGGGCAATCTGCCTTTTGTTAAAGCCTCCAGTGTC 887

Qy 1021 CATTCCATCCCGATGGGGGCATAGTTTGAGACTGCACAGAGAGTGACGTTTTTCTTTAG 1080
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Db 886 CATTCCATCCCTGATGTTGGGGGCAATAGTTTCGAGACTGCAGAGTGACGTTTTTCTTTAG 827

Qy 1081 GGCTGGAGGGCCAGTTCCCACTCAAAGGCCTTGACATTCAAAACTTCANGCTCCT 1140
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Db 826 GGCTGGAGGGCCAGTTCCCACTCAAAGGCTCCCGCCTTGACATTCAAAACTTCANGCTCCT 767

Qy 1141 GAAAACCATTCTCTGCACGAGAAATTGGCTGGTTCGGCGGCTCGAGTGGCTCRAGTGACT 1200
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Db 766 GAAAACCATTCTCTGCACGAGAAATTGGCTGGTTCGGCGGCTCGAGTGGCTCRAGTGACT 707

Qy 1201 CGAGACTCAAATGACTAGGACTTAGACTGGGCGGCTCGGCCCTCGCCTCTGAAAAGTGCTTAAGA 1260
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Db 706 CGAGACTCAAATGACTAGGACTTAGACTGGGCGGCTCGGCCCTCGCCTCTGAAAAGTGCTTAAGA 647

Qy 1261 AAATCTTCTCAGTTCTCCTTGCAGAGGACTGGGGCCGGGAGACCAACGGGGCGCT 1320
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Db 646 AAATCTTCTCAGTTCTCCTTGCAGAGGACTGGGGCCGGGAGACCAACGGGGCGCT 587

Qy 1321 GCACAAAGCGGGCGCGTGTCGGGTGGGTTGGAGTGGAGTACGGGCGGACGGGAAACTGGT 1380
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 586 GCACAAAGCGGGCGCGTGTCGGGTGGGTTGGAGTGGAGTACGGGCGGACGGGAAACTGGT 527

Qy 1381 TGGCGTGCTGCGACGACAGGCGGGCGACGAACACCCGGAAACTGCT 1440
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Db 526 TGGCGTGCTGCGACGACAGGCGGGCGACGAACACCCGGAAACTGCT 467

Qy 1441 GCGAGGACACCGTCTACAGGAGCGGGTTGATGACCGAGTGAGGTAGAAAAACGTCTCCG 1500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 466 GCGAGGACACCGTCTACAGGAGCGGGTTGATGACCGAGTGAGGTAGAAAAACGTCTCCG 407

Qy 1501 AGAAGGGGAGGAGGAGGATCAGTGTACCGCCGGAAGTAGGACCTCGGCCGAGTCGTGCTTGGGTT 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 406 AGAAGGGGAGGAGGAGGATCAGTGTACCGCCGGAAGTAGGACCTCGGCCGAGTCGTGCTTGGGTT 347

Qy 1561 TGGGCGGCAGCCATGAATCCTCCGGAATCTGTTTGGGCATCAGCATACGGACGGCAATGTGCACA 1620
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Qy 1741 GCCAGGAAATGGTACCAAATTTTTCAGTGTTGGACTTGACAGCTTCTTTTGCCACAAGCAA 1800
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Db 166 GCCAGGAAATGGTACCAAATTTTTCAGTGTTGGACTTGACAGCTTCTTTTGCCACAAGCAA 107

Qy 1801 GAGAGAAATTTAACACTGTTTTCAAACCCGCGGGGGGGGGAGTTGGGTGTGTTTAAAGAAAAGAACCATTA 1860
         |||||||||||||||||||||||||||||||||||||||||||||||||| | |
Db 106 GAGAGAAATTTAACACTGTTTTCAAACCCGCGGGGGGGGGAGTTGGGTGTGTTTAAAGAAAAGAACCATTA 47

Qy 1861 AATGCTTTAGACACTGTGAAAAAAA 1884
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Db 46 AATGCTTTAGACAGTGTATTTAAA 23

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RESULT 11
US-09-699-997-11085/c
Sequence 11085, Application US/09699997
GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A.J.
;  APPLICANT: Silos-Santiago, Inmaculada
;  APPLICANT: DiStefano, Peter
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION: THEREFOR
;  FILE REFERENCE: 1600.2020-001
;  CURRENT APPLICATION NUMBER: US/09/699,997
;  CURRENT FILING DATE: 2000-10-30
;  PRIOR APPLICATION NUMBER: 60/162,359
;  PRIOR FILING DATE: 1999-10-29
;  NUMBER OF SEQ ID NOS: 12714
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 11085
;  LENGTH: 1925
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-699-997-11085

Query Match    98.2%;  Score 1863.2;  DB 27;  Length 1925;
Best Local Similarity  99.6%;  Pred. No. 0;
Matches 1876;  Conservative  2;  Mismatches  5;  Indels  1;  Gaps  1;
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Qy      1 GCCAACTCCGGAGGCCTCTGGTGCTCCGGCCCCCGGACGCGGAGGAGCAGACCCG     60
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Db   1905 GCCAACTCCGGAGGCGC-GGTGCTCGGCCCCGGGCCCGGGAGGAGCAGACCCG   1847

Qy     61 CAGCCGGGAGCCCGAGCCGCGGGGCCGATGCAGGCTCCGGCACCTCCTCTA    120
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Db   1846 CAGCCGGGAGCCCGAGCCGCGGGGCCGATGCAGGCTCCGGCACCTCCTCTA   1787

Qy    121 AGCTACGACCGTCGTCTCCGCGGCAGCACGCGGGGCCCAGCAGCCGCCACAGC    180
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Db   1786 AGCTACGACCGTCGTCTCCGCGGCAGCACGCGGGGCCCAGCAGCCGCCACAGC   1727

Qy    181 CGCTGCAGCCGCGGGGCAGCGCCTCCGCGTGTCGCCGCCTTGCCCCTCTCCCG    240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1726 CGCTGCAGCCGCGGGGCAGCGCCTCCGCGTCGCCGCCTTGCCCCTCTCCCG   1667

Qy    241 GCCCCGGGGACTCCCGGACAGAATGTGGGTCCTAGGCATCGCGGGCAACTTTTTTGCGGATTGTT    300
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Db   1666 GCCCCGGGGACTCCCGGAGAATGTGGGTCCTAGGCATCGCGGGCAACTTTTTGCGGATTGTT    607

Qy    301 CTTGCTTCCAGGCTTTGCGCTGCAAAATCCAGTGCTACCAGTGTGAAGAGAATTCCAGCTGAA    360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1606 CTTGCTTCCAGGCTTTGCGCTGCAAAATCCAGTGCTACCAGTGTGAAGAGAATTCCAGCTGAA   1547

Qy    361 CAACGACTGCTCCTCCCCCCGGAGTTCATTGTGAATTGCAGACATGTG    420
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Db   1546 CAACGACTGCTCCTCCCCCGAGTTCATTGTGAATTGCAGACATGTG   1487

Qy    421 TCAGAAGAAGTGATGGAGCAAAAGTGCCGGGATCATGTACCGGAAGTCC    480
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1486 TCAGAAAGAAGTGATGGAGCAAAAGTGCCGGGATCATGTACCGGAAGTCC   1427

Qy    481 AGCGGCCTGTCTCATGGCCCTTGTCCCGGGTACCAGTCCTTCTCCCAGGGAAACTGAA    540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1426 AGCGGGCCTGTCTCATGGCCCTTGTCCCGGGTACCAGTCCTTCTCCCAGGGAAACTGAA   1367

Qy    541 CTCAGTTTGCATCAGCTGCTGCAACACCCCTCTTTGTTAAGGACCCAAGCCAA    600
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Db   1366 CTCAGTTTGCATCAGCTGCTGCAACACCCCTCTTTGTTAACCGGCCCAAGCAAAG   1307

Qy    601 GGGAAGTTCTGCCTCCGGCCCTCAGGCCCAGGGGCCAGGGGCCAGGGAGTTCCTCAAATT    660
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Db   1306 GGGAAGTTCTGCCTCCGGCCCTCAGGCCCAGGGGCCAGGGGCCAGGGAGTTCCTCAAATT    660

Qy    661 AGCCCTCTTCTCGGCACACTGCTTGAACGTGAAGGAGAGATGGCCACCCCCTCCTTGGTTC    720
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Db   1306 AGCCCTCTTCTCGGCACACTGCTGAACGTGAAGGAGAGATGGCCACCCCCTCCTTGGTTC    720

Qy    721 TTCCAGCCCTCGCCCCGCCCCAAACCCCCACCTCCCTCGAGTGAGGTGGAGTTTCTTCTTTT    780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1246 TTCCAGCCCTCGCCCCGCCCCAAACCCCCACCTCCCTCGAGTGAGGTGGAGTTTCTTCTTTT   1187

Qy    781 ATTTCTGGGTAGGGAGGGAGTGGCCGTGTTCTCTTGTTCCTGTTTGTCAAATAATGAAAGAG    840
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Db   1186 ATTTCTGGGTAGGGACGGGAGTCCGGTGTTCTCTTGTTCCTGTTTGTCAAATAATGAAAGAG   1127

Qy    841 CTCGGTGTAAAGGCATTCTGAATAAATTCAGCGTTGACTGAATTTTCAGTATGTACTTGAAGGA    900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1126 CTCGGTAAAGGCATTCTGAATAAATTCAGCTTGACTGAATTTTCAGTATGTACTTGAAGGA   1067

Qy    901 AGGAGGTGGAGTGAAAGTTCACCCCCATGTCTGTGTTGTTGTTTTTGTTTCCTGTGCAAATAATGAAAGAG    960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1066 CTCGGTAAAGCATTCGAATAAATTCAGCTTGACTGAATTTTCAGTATGTACTTGAAGGA   1007

Qy    961 AGAGTCWGTCCTTAGAAGTCACTGAGGTGGGCATCTCCCTTTTGTAAAGGCCTCCAGTGTC    960
          ||||||||: |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1006 AGGAGGTGGAGTGAAAAGTTCACCCCCATGTCTGTGTAACCGGAGTCAAGGCTGGC    947

Qy   1021 CAATTCCATCCCCTGATGGGGGGGCATAGTTGTTGAGGACTGCAGAGTGAGAGTGACGTTTTTTCTTAG   1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    946 AGAGTCAGTCCTTAGAAGTCACTGAGGTGGGCATCTCCCTTTTGTAAAGGCCTCCAGTGTC    887

Qy   1081 GGCTGGAGGGGCCAGTTCCCACTCAAGGCTCCCCTCGCGTTGCTTGTTGACATTCAAAACTTCATGCTCCT   1140
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Db    886 CATTCCATCCCCTGATGGGGGGGCATAGTTGTTGAGGACTGCAGAGTGAGAGTGACGTTTCTTAG    827

Qy   1141 GAAAACCATTCTCTTCCCAGCACGAAATTGGCTGGTTTCCGGCTTGGGCTTCTAGTGACT   1200
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Db    826 GGCTGGAGGGGCCAGTTCCCACTCAAGGCTCCCCTCGCGTTGCTTGTTGACATTCAAAACTTCATGCTCCT    767

Qy   1201 CGAGACTCAATGACTTAGACTGGGACTTAGACTGGGGCCTCGGCTCTGAAAAGTGCTTAAGA   1260
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Db    766 GAAAACCATTCTCTTCCCAGCACGAAATTGGCTGGTTTCCGGCTTGGGCTTCTAGTGACT    707

Qy   1261 AAATCTTCTCAGTTGTCCTTGCAGAGGACTGGGGCGGGACCGGACGCAACGGGGGGGGCT   1320
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Db    706 CGAGACTCAATGACTTAGACTGGGACTTAGACTGGGGCCTCGGCTCTGAAAAGTGCTTAAGA    647

Qy   1321 GCACAAAAGCGGGCGGCGTGTCGGTGTGTGAGTCCGCATGTACCGCGACCGGACCGGGTGGT   1380
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Db    646 AAATCTTCTCAGTTGTCCTTGCAGAGGACTGGGGCGGGACCGGACGCAACGGGGGGGCT    587

Qy   1381 TGGCCGTGCTGCAGCGACACAGGCCAGCACACACCGCACGAACACCGCCGGAAACTGCT   1440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    586 GCACAAAAGCGGGCGGCGTGTCGGTGTGTGAGTCCGCATGTACCGCGACCGGACCGGGGT    527

Qy   1441 GCGAGGACACCGTGTACAGGAGCGGGGTTGATGACCGGACCTGAGGTGTAGAAAAACGTCTCCG   1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    526 TGGCCGTGCTGCAGCGACACAGGCCAGCACACACCGCACGAACACCGCCGGAAACTGCT    467
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Db    346 TGGCCGCGCAGCCATGATCCTCCGAATCTGGTTGGGCATCCACCACTACGGCGCCAATGTCACAA    287
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Qy   1621 CAATCAGCCCTGGGCGAGACACGAGCGAGGAGGAGGAGGAGGAGAAGAAAAACACAGCAT   1680

Db    286 CAATCAGCCCTGGGCGAGACACGAGGAGGAGGAGGAGGAGAAGAAAAACACAGCAT    227
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Qy   1681 GAGAACACAGTAAATAAATATAAAATATTTTAGCCCCTCTCGTTCTGTGCTTACTG   1740

Db    226 GAGAACACAGTAAATAAATATAAAATATTTTAGCCCCTCTCGTTCTGTGCTTACTG    167
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Qy   1741 GCCAGGAAAATGGTACCCAATTTTTCAGTGTTGTTGGACTTGACAGCTTCTTTTGCCACAAGCCAA   1800

Db    166 GCCAGGAAAATGGTACCCAATTTTTCAGTGTTGTTGGACTTGACAGCTTCTTTTTGCCACAAGCCAA    107
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1801 GAGAGAAATTAACACTGTTTCAAACCCGGGGGAGTTGGGCTGTGTTGTTAAAGAAAGACCATTA   1860

Db    106 GAGAGAAATTAACACTGTTTCAAACCCGGGGGGAGTTGGGCTGTGTTGTTAAAGAAAGACCATTA    47
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1861 AATGCTTTAGACAGTGTAAAAAAA   1884

Db     46 AATGCTTTAGACAGTGTATTTAA   23
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RESULT 12
US-09-710-281-4458/c
Sequence 4458, Application US/09710281
GENERAL INFORMATION:
 APPLICANT:  Hunter, John J.
 APPLICANT:  Shyjan, Andrew W.
 APPLICANT:  Stdal, Hilde
 TITLE OF INVENTION:  NOVEL NUCLEIC ACID MOLECULES AND USES
 TITLE OF INVENTION:  THEREFOR
 FILE REFERENCE:  1600.2036-001
 CURRENT APPLICATION NUMBER:  US/09/710,281
 CURRENT FILING DATE:  2000-11-10
 PRIOR APPLICATION NUMBER:  60/164,254
 PRIOR FILING DATE:  1999-11-09
 NUMBER OF SEQ ID NOS:  5803
 SOFTWARE:  FastSEQ for Windows Version 4.0
 SEQ ID NO 4458
 LENGTH: 1925
 TYPE: DNA
 ORGANISM: Homo sapiens
US-09-710-281-4458

 Query Match   98.2%;  Score 1863.2;  DB 28;  Length 1925;
 Best Local Similarity  99.6%;  Pred No. 0;
 Matches 1876;  Conservative  2;  Mismatches  5;  Indels  1;  Gaps  1;
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Qy      1 GCCAACTCCGGAGGCTCTGGTGCTCGGCCCGGAGCGCGGAGCGCGGAGCAGAGACCCG 60
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Db   1905 GCCAACTCCGGAGGCGC--GGTGCTCGGGCCCGGGAGCGCGGAGGCAGAGACCCG 1847

Qy     61 CAGCCGGGGGAGCCCGAGCGCGGGGATGCAGGCCGCACCTCGGCGTCCTCTA 120
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Db   1846 CAGCCGGGGGAGCCCGGGATCGCAGGCCGCCACCTCGGCGTCCTCTA 1787

Qy    121 AGCTACGACCGTGTCTCCGCGGCAGCAGCCCGGCAGCGGCAGCCACAGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1786 AGCTACGACCGTGTCTCCGCGGCAGCAGCCCGGCAGCGGCAGCCACAGC 1727

Qy    181 CGCTGCACCCGGCCAGCCTCCCGTGTCTGTCGCGCTGATCGCGCTCCTCTGATCCGG 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1726 CGCTGCACCCGGCCAGCCTCCCGTGTCTGTCGCGCCTCCTCTGATGCGCTTGCCCTCTCCG 1667

Qy    241 GCCCCGGGGGACTCCGGGAGCTCCGGGAGAATGTGGGGTTCCTAGGCATGCGGGGCATGCGGGCAACTTTTTGCGGATTGTT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1666 GCCCCGGGGGGACTCCGGGAGACTCCGGGAGAATGTGGGGTCCTAGGCATCGGGGCAACTTTTTGCGGATTGTT 1607

Qy    301 CTTGCTTCCAGGCGTTTGCGCGTGCAAAATCCAGTGCTGACCGTACCAGTGTGAGAGAAGAATTCCAGCTGAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1606 CTTGCTTGCAGGCGTTTGCGCGTGCAAAATCCAGTGCTGACCGTACCAGTGTGAGAGAAGAATTCCAGCTGAA 1547

Qy    361 CAACGACTGCTCCTCCCCCGGAGTTCATTGTGAAATTGCACGGTGAACGTTCAAAGACATGTG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1546 CAACGACTGCTCCTCCCCCGGAGTTCATTGTGAAATTGCACGGTGAACGTTCAAAGACATGTG 1487

Qy    421 TCAGAAAAGAAGTGATTGGAGGAGAAAGTGCCCGGGATCATGTACCGCGAAGTCCGTTGCATCATC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1486 TCAGAAAAGAAGTGATTGGAGGAGAAAGTGCCCGGGATCATGTACCGCGAAGTCCGTTGCATCATC 1427

Qy    481 AGCGGCCGTGTCTCATCGCCGCTCTCGCGGGTACCAGTGCCTTCTTGCTCGTGCCGGGAAACTGAA 540
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Db   1426 AGCGGCCGTGCTCATCGCCGCTCTCGCGGGTACCAGTGCCTTCTTGCTCGTGCCGGGAAACTGAA 1367

Qy    541 CTCAGTTTGCATCAGCTGGTGCACACACCCCTCTCTTTGTTACGGGGTACTATTGTTACTCGAAGGA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1366 CTCAGTTTGCATCAGCTGCTGCAACACCCCCTCTTTGTTAACGGGCAGGGAAACAGACCATTA 1307

Qy    601 GGGAAGTTCTGCCTCGGGCCTCAGCCACCAGGGGCTCCGCCACCACCATCCTGTTCCTCAAATT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1306 GGGAAGTTCTGCCTCGGGCCTCAGCCACCAGGGGCTCCGCCACCACCATCCTGTTCCTCAAATT 1247

Qy    661 AGCCCTCTTCTCGGCCACATGCTGAAGCGTGAAAGGAGCTGAAGGAGAATGCCACCCCTCCTTGCATTGTTC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1246 AGCCCTCTTCTCGGCCACATGCTGAAGCGTGAAAGGAGAGAATGCCACCCCTCCTTGCATTGTTC 1187

Qy    721 TTCCAGCCCTCGCCCCAACCCCACCCCTCCCTGAGTGAGTTCTTCTGGGTGTCCTTTT 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1186 TTCCAGCCCTCGCCCCAACCCCACCCCTCCCTGAGTGAGTTCTTCTGGGTGTCCTTTT 1127

Qy    781 ATTCTCGGGTAGGGACGGGAGTCCGTGTTCTCTTTTGTTCCTTGTGCCAAATAATGAAAGAG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1126 ATTCTCGGGTAGGGACGGGAGTCCGTGTTCTCTTTTGTTCCTTGTGCCAAATAATGAAAGAG 1067

Qy    841 CTCGGTAAAGCCATTCTGAATAAAATTCAGCYTGACTGGAATTTTCAGTATTGTACTCGAAGGA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1066 CTCGGTAAAGCCATTCTGAATAAAATTCAGCTTGACTGGAATTTTCAGTATGTACTTGAAGGA 1007

Qy    901 AGGAGGTGGAGTGAAAGTTCACCCCCCATGTCTGTGTAACCGGAGTCAAGGCCAGGCTGGC 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1006 AGGAGGTGGAGTGAAAGTTCACCCCCCATGTCTGTGTAACCGGAGTCAAGGCCAGGCTGGC 947

Qy    961 AGAGTCWGTCCTTAGAGTCACTGAGGTGGGCCATCTGCCTTTTGTAAAGCCTCCAGTGTC 1020
          |||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    946 AGAGTCAGTCCTTAGAGTCACTGAGGTGGGCATCTGCCTTTTGTAAAGCCTCCAGTGTC 887

Qy   1021 CATTCCCATCCCCTGATGGGGGGCATAGTTGTTGAGACTGAGAGTGAGAGTTTCTTAG 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    886 CATTCCCATCCCCTGATGGGGCATAGTTTGAGACTGAGAGTGAGACGTTTTCTTAG 827

Qy   1081 GGCTGGAGGGGCCAGTTCCCACTCAAGGCTCCCTCGCTTGACATTCAAAACTTCATGCCTCCT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    826 GGCTGGAGGGGCCAGTTCCCACTCAAGGCTCCCTCGCTTGACATTCAAAACTTCATGCCTCCT 767

Qy   1141 GAAAACCATTCTCTGCAGCACAAATTGGCTGTTTCCGCGTTCAGTTGGGCTCTAGTGACT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    766 GAAAACCATTCTCTGCAGCAGAAATTGGCTGTTTCCGCGTTCAGTTGGGCTCTAGTTGACT 707

Qy   1201 CGAGACTCAATGACTGGGACTTAGACTGGGGCTCGGCGCCTCGGCTGCTCTGAAAAGTGCTTAAGA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    706 CGAGACTCAATGACTGGGACTTAGACTGGGGCTCGGCGCCTCGGCTGCTCTGAAAAGTGCTTAAGA 647

Qy   1261 AAATCTTTCTCAGTTCTCCTTGCCAGAGGACTGGCGGCGGGACGCGCGGGACGGGGCGCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    646 AAATCTTTCTCAGTTCTCCTTGCCAGAGGACTGGCGGCGGGACGCGCGGGACGGGGCGCT 587
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Db    466 GCGAGGACACCGTGTACAGGAGGAGGGTTGATGAGCCCAGCTGAGGTTAGAAAAACGTCTCCG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1501 AGAAGGGGAGGAGGATCATGTTACGGCCCGGGAAGTCCAGTCGTTGCGTTT 1560

Db    406 AGAAGGGGAGGAGGATCATGTTACGCCCGGGGAGTAGGAGTCCAGTCGTTGCTTGGGTT 347

Qy   1561 TGGCCCGCAGCCATGAATCTTCCGAAATCTCGGAATCTCAGCCATACGGCCATTGCACAA 1620

Db    346 TGGCCCGCAGCCATGAATCTCGGAATCTCGGTTGGGCATCACGGCCAATGTCACAA 287

Qy   1621 CAATCAGCCCTGGGCACACACCAGCAGGAGGAGAGAGAGAGAGACACAGCAT 1680

Db    286 CAATCAGCCCTGGGCAGACACCAGCAGGAGGAGAGAGAGAGAGACACAGCAT 227

Qy   1681 GAGAACACAGTAAAATGAAATAAAACCATAAATAATATTTAGCCCCTCCTCTGTTCTCTGCTTACTG 1740

Db    226 GAGAACACAGTAAATAAATAAAAACCATAAATAATATTTAGCCCCTCCTCTGTTCTCTGCTTACTG 167

Qy   1741 GCCAGGAAATGGTACCAAATTTTTCAGTGTGTTGGACTTGACAGCTGTTCTTTTGCCACAAGCAA 1800

Db    166 GCCAGGAAATGGTACCAAATTTTTCAGTGTGTTGGACTTGACAGCTGTTCTTTTGCCACAAGCAA 107

Qy   1801 GAGAGAATTTAACACTGTTTCAAACCCGGGAGTTGGCTGTGTTGTTAAAGAAAGAACCATTA 1860

Db    106 GAGAGAATTTAACACTGTTTCAAACCCGGGGAGTTGGCTGTGTTGTTAAAGAAAGAACCATTA 47

Qy   1861 AATGCTTTAGACAGTGTAAAAAAA 1884

Db     46 AATGCTTTAGACAGTGTATTTAAA 23
```

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Qy   1321  GCACAAAGGCGGCGGGCGGCGTTGCGGTGGGGTGGGAGTGCGCATGTACGCGCAGCGCGCTTCTCGTTGGT  1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    586  GCACAAAGGCGGGCGGGCGGCGTTGCGGTGGGGTGGGAGTGCGCATGTACGCGCAGCGCGCTTCTCGTTGGT  527

Qy   1381  TGGGCTGCTGCCAGCGCACAGCGCGGCACCACAGCCAACACCCGCCGAAACTGCT  1440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    526  TGGGCTGCTGCCAGCGCACAGCGCGGCACCACAGCCAACACCCGCCGAAACTGCT  467

Qy   1441  GCGAGGAACACCGTGTACAGGAGGCGGGTTGATGACCGACACCAGTAGAAAAACGTCTCCG  1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    466  GCGAGGAACACCGTGTACAGGAGGCGGGTTGATGACCGACACCAGTAGAAAAACGTCTCCG  407

Qy   1501  AGAAGGGGAGGAGGATCATGTACGCCCGGGAAGTAGGAGCCTCGTGCCCCGGATT  1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    406  AGAAGGGGAGGAGGATCATGTACGCCCGGGAAGTAGGAGCCTCGTGCCCCGGATT  347

Qy   1561  TGGGCGCCAGCCATGATCCTCCGAATCTGGTTGGGGCATCCACCCCCGGAAGTCACAA  1620
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    346  TGGGCGCCAGCCATGATCCTCCGAATCTGGTTGGGGCATCCACCCCCGGAAGTCACAA  287

Qy   1621  CAATCAGCCCTGGGCAGCACAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGCAGCA  1680
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    286  CAATCAGCCCTGGGCAGCACAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGCAGCA  227

Qy   1681  GAGAACACAGTAAATGAATAAAAACCATAAAAATATTTAGCCCCTGTCTTCTGTGCTTACTG  1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    226  GAGAACACAGTAAATAAATAAAAACCATAAAAATATTTAGCCCCTGTCTTCTGTGCTTACTG  167

Qy   1741  GCCAGGAAATGGTACCAATTTTTCAGTGTTTGACTTGACTTGACAGCTTCTTTTGCCACAAGCCAA  1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    166  GCCAGGAAATGGTACCAATTTTTCAGTGTTGGGACTTGACACAGCTTCTTTTGCCACAAGCCAA  107

Qy   1801  GAGAGAATTTAACACTGTTTCAAACCCGGGGGGAGTTGGGCTGTGTTGTTAAAGAAAGACCATTA  1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    106  GAGAGAATTTAACACTGTTTCAAACCCGGGGGGAGTTGGGCTGTGTTGTTAAAGAAAGACCATTA  47

Qy   1861  AATGCTTTAGACAGTGTAAAAAA  1884
           |||||||||||||||||||
Db     46  AAATGCTTTAGACAGTGTAATTTAA  23
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Query Match   98.2%; Score 1863.2; DB 29; Length 1925;
Best Local Similarity   99.6%; Pred. No. 0;
Matches 1876; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

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Qy     1  GCCAACTCCGGAGGCCTCTGTGCTCGGGCCGCGAGCCGGGACGAGAGACCCG  60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1905  GCCAACTCCGGAGGCCGC--GGTGCTCGGGCCCCGGGAGCCGGGACGAGAGACCCG  1847

Qy    61  CAGCCCGGAGAGCCCGAGGCGGCGGATGCAGAGGCGCGCACCTCGGGCGCTCCTCTA  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1846  CAGCCGGGAGAGCCCGAGGCGGCGGATGCAGAGGCGCGCACCTCGGGCGCTCCTCTA  1787

Qy   121  AGCTACGGACCGTGCGTCTCCGGCGGCGCGCCGGCCGCAGCGCCAGCGCCAGCGCGGCGCCGCACAGC  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1786  AGCTACGGACCGTGCGTCTCCGGCGGCGCGCCGGCCGCAGCGCCAGCGCCAGCGCGGCGCCGCACAGC  1727

Qy   181  CGCTGCAGCCGGCCGGGGCAGCCTCCGGGTGCTGCTTGCCGCTCTCCGGGGCCGGCGGGGCCCCCGG  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1726  CGCTGCAGCCGGCCGGGGCAGCCTCCGGGTGCTGCTTGCCGCTCTCCGGGGCCGGCGGGGCCCCCGG  1667

Qy   241  GCCCCGGGGACTCCGGGGAGAAATGTGGGGTCCTAGGCGCATCGCGGGCATCTTTTGCGGATTGGTT  300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1666  GCCCCGGGGACTCCGGGGAGAAATGTGGGGTCCTAGGCGCATCGCGGGCATCTTTTGCGGATTGGTT  1607

Qy   301  CTTGCTTCCAGGCGCTTTGCGCCTGCAAATCCAGTGCTACCAGTGCGCGGAGAATTCCAGCTGAA  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1606  CTTGCTTCCAGGCTTTGCGCCTGCAAATCCAGTGGTCCTAGGCATGCGCGGAGAATTCCAGCTGAA  1547

Qy   361  CAACGACTGCTCCTCCCCCGAGTTCATTTGGTGAATTGCAGCGGTGAACGTTCAAGACATGTG  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1546  CAACGACTGCTCCTCCCCCGAGTTCATTTGGTGATTGGAGCAAAGTGCCGGGATCATGTGCATCATC  1487

Qy   421  TCAGAAAGAAGAGTGAGTGGAGCAAAAGTTCCCGGGATCATCAGTCTACCCGGAAGTCCTTGCATCATC  480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1486  TCAGAAAGAAGAGTGAGTGGAGCAAAAGTTCCCGGGATCATCAGTCTACCCGGAAGTCCTTGCATCATC  1427

Qy   481  AGCCGGCCTGTCTCATCGGCCTTCTGGCCAACACCCCCTCTTGTAACGGGCCAAGAAAAG  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1426  AGCCGGCCTGTCTCATCGGCCTTCTGGCCAACACCCCCTCTTGTAACGGGCCAAGAAAAG  1367

Qy   541  CTCAGTTTGCATCAGCGTGCTGCGAACAACACCCTCTTTGTTGTAACGGGCCAAGAAAACTGAA  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1366  CTCAGTTTGCATCAGCGTGCTGCGAACAACACCCTCTTTGTTGTAACGGGCCAAGAAAACTGAA  1307

Qy   601  GGGAAGTTCTGCCTCGGCCCCTCCAGGCCGCAGGCGCTCCCCACCACCATCTCTGTTCTCAAATT  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1306  GGGAAGTTCTGCCTCGGCCCCTCCAGGCCGCAGGCGCTCCCCACCACCATCTCTGTTCTCAAATT  1247

Qy   661  AGCCCTCTTCTCGGCACACTCCTGAAGCTGAAGGAGGAGGAGGATGCCACCCCGTTGCATTGTTC  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1246  AGCCCTCTTCTCGGCACACTCCTGAAGCTGAAGGAGGAGGAGGATGCCACCCCGTTGCATTGTTC  1187

Qy   721  TTCCAGCCCTCGCCCCCCACCTCCCTGAGTGAGTTTCTTCTGGGGTGTCCTTTT  780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1186  TTCCAGCCCTCGCCCCCCACCTCCCTGAGTGAGTTTCTTCTGGGGTGTCCTTTT  1127

Qy   781  ATTCTGGGTAGGGAGGGGACTGCCTCGGTGTTCTCTGTGGCAAATAATAATGAGAGAGAGAG  840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1126  ATTCTGGGTAGGGAGGGGACTGCCTCGGTGTTCTCTGTGGCAAATAATGAGAGAGAG  1067

Qy   841  CTCCGTAAAGCCATTCTGAAATAATTCAGCYTGACTGAATTTTCAGTATGTACTTGAAGGA  900
          ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db  1066  CTCCGTAAAGCCATTCTGAAATAAATTCAGCTTGACTGAATTTTCAGTATGTACTTGAAGGA  1007

Qy   901  AGGAGGTGGAGTGAAGTTCACCCCATGTCTGTGTGTAACCGGAGTCAAGGCCAGGCTGGC  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1006  AGGAGGTGGAGTGAAGTTCACCCCATGTCTGTGTGTAACCGGAGTCAAGGCCAGGCTGGC  947

Qy   961  AGAGTGCWGTCCTTAGAAGTGACTGACTGAGGTGGGCATCTGCCCTTTTGTAAAGCCTCCAGTGTC  1020
          ||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    946  AGAGTCAGTCCTTAGAAGTGACTGACTGAGGTGGGCATCTGCCCTTTTGTAAAGCCTCCAGTGTC  887

Qy  1021  CATTCCATCCCTGATGGGGGCCCATAGTTTGTGAGACTGCAGAGTGACGAGTGAGCGTTTTCTTAG  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    886  CATTCCATCCCTGATGGGGGCCCATAGTTTGTGAGACTGCAGAGTGACGAGTGAGCGTTTTCTTAG  827

Qy  1081  GGCTGGAGGGGCCAGTTCCCACTCAAGGCTCCCGCTTGACATTCAAAACTTCATNGCTTCT  1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    826  GGCTGGAGGGGCCAGTTCCCACTCAAGGCTCCCGCTTGACATTCAAAACTTCATNGCTTCT  767

Qy  1141  GAAAACCATTCTCTGCAGCAGAATTGGCTGGTTTCGGCGCCTGAGTTGGGGCTCTAGTGACT  1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    766  GAAAACCATTCTCTGCAGCAGAATTGGCTGGTTTCGGCGCCTGAGTTGGGGCTCTAGTGACT  707
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Query Match   97.6%;   Score 1851;   DB 17;   Length 1917;
Best Local Similarity 99.7%;   Pred. No. 0;

US-09-371-168-7188
SEQ ID NO 7188
  LENGTH: 1917
  TYPE: DNA
  ORGANISM: Homo sapiens
  SOFTWARE: FastSEQ for Windows Version 3.0
  NUMBER OF SEQ ID NOS: 8285
  EARLIER FILING DATE: 1998-10-05
  EARLIER APPLICATION NUMBER: 60/103,145
  EARLIER FILING DATE: 1998-08-10
  EARLIER APPLICATION NUMBER: 60/095,907
  CURRENT FILING DATE: 1999-08-10
  CURRENT APPLICATION NUMBER: US/09/371,168
  FILE REFERENCE: MLN98-37pA
  TITLE OF INVENTION: HUMAN BRAIN LIBRARY
  TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
  APPLICANT: Glucksmann, M. Alexandra
GENERAL INFORMATION:
  Sequence 7188, Application US/09371168
US-09-371-168-7188

RESULT 14

Matches 1873; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

```
Qy     1 GCCAACTCCGCAGGGCTTCTGGTTGCTCGGAGGCGCGGGAGCGGAGCGGGAGGAGGAGAGACCCG    60
         ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db    46 GCCAACTCCGGAGGGCTTCTGGTTGCTCGGAGGCGCGGG-GGTGCTCGGGGAGCGGAGCGGGAGGAGGAGAGACCCG   74

Qy    61 CAGCCGGGGAGCCCCCAGAGCGGGGGGCCCAATGCAGGTCCGGGACCTCCTCTA   120
Db    75 CAGCCGGGGAGCCCGAGCGGGGGGCCCAATGCAGGTCCGGGACCTCCTCTA    134

Qy   121 AGCTACGACCGTCGTCTCCCGGGAGAATGCAGCAGCAGCAGCCACAGC    180
Db   135 AGCTACGACCGTCGTCTCCCGGGAGAATGTGGGGTCCTAGGCAGCCACAGC    194

Qy   181 CGCTGCAGCCCGGGGGCCAGCCTCGGCGTCGTCGCCGGGGGCCTGCCCTCTCCCG    240
Db   195 CGCTGCAGCCCGGGGGCCAGCCTCGGCGTCGTCGCCGGGGCCTGCCCTCTCCCG    254

Qy   241 GCCCCGGGGACTCCGGGAGAAATGTGGGGTCCTAGGCACGCGCGCAACTTTTTGCCGGATTGTT    300
Db   255 GCCCCGGGGACTCCGGGAGAATGTGGGGTCCTAGGCACGCGCGCAACTTTTTGCCGGATTGTT    314

Qy   301 CTTGCTTCCAGGCTTTGCCGCTGCAAATCCAGTGTCTACCAGTGTGCAAGAATTCCAGCT-GA    359
Db   315 CTTTGCTTCCAGGCTTTGCCGCTGCAAATCCAGTGTCTACCAGTGTGCAAGAATTCCAGCTGA    374

Qy   360 ACAACGACTGGTCTCTCCCCGGGAGGTCAATGGGCCAAATGTCACAG    419
Db   375 ACAACGACTGCTCTCTCCCCGGGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGT    434

Qy   420 GTCAGAAAAGAAGTGATTGGGGAGAAATGCCGGGAGTCATGTACCGCAAGTCCTGTGTGCATCAT    479
Db   435 GTCAGAAAGAGAAGTGATTGGGGAGAAATGCCGGGAGTCATGTACCGCAAGTCCTGTGTGCATCAT    494

Qy   480 CAGCGCGCCTGTTCTCATCGCCTTCTGCCTCTGCTCCCCAGGGAAACTGA    539
Db   495 CAGCGCGCCTGTTCTCATCGCCTTCTGCCTCTGCTCCCCAGGGAAACTGA    554

Qy   540 ACTCAGTTGCATCAGCTGCTGCACACCCCTCTTTGTGTAACGGGCCAAGAAAA    599
Db   555 ACTCAGTTTGCATCAGCTGCTGCACACCCCTCTTTGTGTAACGGGCCAAGAAAA    614

Qy   600 GGGGAAGGTTCTGGCCTCGGCCCCTCAGGCCAGGGGCTCCGCACCATCCTGTTCCTCAAAT    659
Db   615 GGGGAAGGTTCTGGCCTCGGCCCCTCAGGCCAGGGGCTCCGCACCATCCTGTTCCTCAAAT    674

Qy   660 TAGCCCCTCTTCTCGGCACACTGCTGAAGCTGAAGGAGGATGGCCACCCCTCCTGCATTGTT    719
Db   675 TAGCCCCTCTTCTCGGCACACTGCTGAAGCTGAAGGAGGATGGCCACCCCTCCTGCATTGTT    734

Qy   720 CTTCCAGCCCTCTCGCCCCCACCCCACCTCCCTGAGTGACTTTCTTCTTTGGGTGTCCTTT    779
Db   735 CTTCCAGCCCTCTCGCCCCCAACCCCACCTCCCTGAGTGACTTTCTTCTTTGGGTGTCCTTT    794

Qy   780 TATTCTGGGGTAGGGAGGACGGGGGAGTCCGTGTTCTCTCTTTTGGTTCCTGGGCAAAATAATGAAAGA    839
Db   795 TATTCTGGGGTAGGGAGGACGGGGGAGTCCGTGTTCTCTCTTTTGGTTCCTGGGCAAAATAATGAAAGA    854

Qy   840 GCTCGGTAAAGCATTCTGAATAAATTCAGCYGACTGAAATTTTCAGTATGTTACTTGAAGG    899
Db   855 GCTCGGTAAAGCATTCTGAATAAATTCAGCTGACTGAAATTTTCAGTATGTGTACTTGAAGG    914

Qy   900 AAGGAGGTGGAGTGAAAGTTCACCCCCATGTCTGTGTGTAACCGGAGTGCAAGGCGCTGG    959
Db   915 AAGGAGGTGGAGTGAAAGTTCACCCCCATGTCTGTGTGTAACCGGAGTGCAAGGCCAGGCTGG    974

Qy   960 CAGAGTCWGTCCTTAGAAGTCACTGAGGTGGGCCATCTGCCTTTTGTTAAAGGCCTCAGTGT    1019
Db   975 CAGAGTCAGTCCTTAGAAGTCACTGAGGTGGGCCATCTGCCTTTTGTTAAAGGCCTCAGTGT    1034

Qy  1020 CCATTCCATCCCTGATTGGGGGGCATAGTTTGAGACTGCAGAGTGAGAGTGAGGTTTTCTTA    1079
Db  1035 CCATTCCATCCCTGATTGGGGGGCATAGTTTGAGACTGCAGAGTGAGAGTGAGGTTTTCTTA    1094

Qy  1201 CGAGACTCAATGACTGGGACTTAGACTGGGGCTTCGGGCTTCGCCTCTGAAAAGTGCTTAAGA    1260
Db   646 CGAGACTCAATGACTGGGACTTAGACTGGGGCTTCGGGCTTCGCCTCTGAAAAGTGCTTAAGA    647

Qy  1261 AAATCTTCTCAGTTCTCCTTGCAGAGAGACTGGCGCGGGAGGCGGAAGAGCAACGGGGCGCT    1320
Db   587 AAATCTTCTCAGTTCTCCTTGCAGAGAGACTGGCGCGGGAGGCGGAAGAGCAACGGGGCGCT    587

Qy  1321 GCACAAAGCGGCGCGCTGTCGGGTGGTGAGTGCGCCATGTACCGCGGGCGGCTTCTCTGGT    1380
Db   586 GCACAAAGCGGGGCGCGCTGTCGGGTGGTGGAGTGCGCCATGTACCGCGGGCGGCTTCTCTGGT    587

Qy  1381 TGGCGTGCTGCAGCGCGACGAGGCGGCAGCAGCACGCCACCGGCGGCAGAGGAGAAACTGCT    1440
Db   527 TGGCGTGCTGCAGCGCGACGAGGCGGCAGCAGCACGCCACCGGCGGCAGAGGAGAAACTGCT    527

Qy  1441 GCGGAGGACACCGTGTACAGGAGACGGGGTTGATGACCGAGCTGAGGTAGAAGAACGTCTCCG    1500
Db   466 GCGGAGGACACCGTGTACAGGAGACGGGGTTGATGACCGAGCTGAGGTAGAAGAACGTCTCCG    467

Qy  1501 AGAAGGGGAGGAGGATCATGTACGCCCGGGAAGTAGGAGGCCACCCAGTGTCGTGCTTGGGTT    1560
Db   406 AGAAGGGGAGGAGGATCATGTACGCCCGGGAAGTAGGAGGCCACCCAGTGTCGTGCTTGGGTT    407

Qy  1561 TGGCCCGCAGCCATGATCTCTCCCAAATCGTGGTTGGGCATCCCAGTATACGCCCAATGTCACAA    1620
Db   346 TGGCCCGCAGCCATGATCTCTCCCAAATCGTGGTTGGGCATCCCAGTATACGCCCAATGTCACAA    347

Qy  1621 CAATCAGCCTGGCAGACACGACAGCAGGAGAGAGAGAAAAAACACAGCAT    1680
Db   286 CAATCAGCCCTGGGCAGACACGACAGCAGGAGAGAGAGAAAAAAACACAGCAT    227

Qy  1681 GAGAACACAGTAAAATGAATAAAAACCATAAAAATATTAGCCCCTCGTTCTGTTGCTTACTG    1740
Db   226 GAGAACACAGTAAAATAAAAACCATAAAAATATTAGCCCCTCTGTTCTGTTGCTTACTG    167

Qy  1741 GCCAGGAAATGGTACCAAATTTTTCAGTGTTGGACTTGACAGCTTCTTTTGCCACAAGCAA    1800
Db   166 GCCAGGAAATGGTACCAAATTTTTCAGTGTTGGACTTGACAGCTTCTTTTGCCACAAGCAA    107

Qy  1801 GAGAGAAATTTAACACTGTTTCAAACCCGGGGAGTTGGCTGTGTTGTTAAAGAGAAAGACCATTA    1860
Db   106 GAGAGAAATTTAACACTGTTTCAAACCCGGGGGAGTTGGCTGTGTTGTTAAAGAGAAAGACCATTA    47

Qy  1861 AATGCTTTAGACAGTGTAAAAAAA    1884
Db    46 AATGCTTTAGACAGTGTATTTAAA    23
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RESULT 15
US-09-644-873-9077
Sequence 9077, Application US/0964473
GENERAL INFORMATION:
    APPLICANT: Silos-Santiago, Inmaculada
    APPLICANT: Holtzman, Douglas A.
    TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
    TITLE OF INVENTION: THEREFOR
    FILE REFERENCE: 1600.1169-001
    CURRENT APPLICATION NUMBER: US-09/644,873
    CURRENT FILING DATE: 2000-08-28
    PRIOR APPLICATION NUMBER: 60/151,064
    PRIOR FILING DATE: 1999-08-27
    NUMBER OF SEQ ID NOS: 11286
    SOFTWARE: FastSEQ for Windows Version 4.0

    SEQ ID NO 9077
    LENGTH: 1917
    TYPE: DNA
    ORGANISM: Homo sapiens
US-09-644-873-9077

Query Match             97.6%;  Score 1851;  DB 25;  Length 1917;
Best Local Similarity   99.7%;  Pred. No. 0;
Matches 1873;  Conservative  2;  Mismatches  2;  Indels  2;  Gaps  2;
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Qy    1080 GGGCTGGAGGGCCAGTTCCCACTCAAGGCTCCTCCTCGCTTGACATTCAAACTTCATGTCC 1139
           ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    1095 GGGCTGGAGGGCCAGTTCCCACTCAAGGCTCCCCCTCGCTTGACATTCAAACTTCATGTCC 1154

Qy    1140 TGAAAACCATTCTCTGCAGCAGAATTGGCTGTGGTTTCGGCCGCCTTGAGTTGGGCTCTAGT 1199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1155 TGAAAACCATTCTCTGCAGCAGAATTGGCTGTGGTTTCCCGCCTTGAGTTGGGCTCTAGTGAC 1214

Qy    1200 TCGAGACTCAATGACTAGACTGGGGACTTAGACTGGGGCTCGGGCTCTGAAAAAGTGCTTAAG 1259
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Db    1215 TCGAGACTCAATGACTAGACTGGGGACTTAGACTGGGGCTCGGGCTCTGAAAAGTGCTTAAG 1274

Qy    1260 AAAATCTTCTCAGTTCTCCTTGCAGAGGACTGGGGCGCGCGGGAAGCAACGGGCGC 1319
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Qy    1320 TGCACAAAAGCGGGCGGCGCCGTGTGTGGTGTGCATGTACGGCGGGGAAGAGCAACGGGCGC 1379
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Qy    1440 TGCGGAGGGACACCGTGTACAGGAGCGGGTTGATGAGCGCGTGGAGGTAGGTGAGAAACGTGTCC 1499
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Qy    1620 ACAATCAGCCCTGGGCAGACGAGCGAGAGCGAGAGCGAAAATGTCAGA 1679
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Qy    1740 GGCCAGGGAAATGGTACCAATTTTTTCAGTGTTGGACTTGACAGCTTCTTTTTCCACAAGCA 1799
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Db    1755 GGCCAGGGAAATGGTACCAATTTTTCAGTGTTGGACTTGACAGCTTCTTTTCCACAAGCA 1814

Qy    1800 AGAGAGAATTTAACACTGTTTCAAACCCGGGAGTTGGCTGGTGTGTTGTTAAAGAAAGACCATT 1859
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Db    1815 AGAGAGAATTTAACACTGTTTCAAACCCGGGAGTTGGCTGTGTGTTAAAGAAAGACCATT 1874

Qy    1860 AAATGCTTTAGACAGTGTA 1878
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Db    1875 AAATGCTTTAGACAGTGTA 1893
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Qy      61 CAGCCGGGAGCCCGAGCCGCCGGAGGCGGCTCGGCCGAGCCTCCGGCCACCACCAGC 120
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Qy     181 CGCTGCAGCCCGGGCAGCCCTCCGGCGGCGGCTTGCCCTTCTCCCG 240
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Db     195 CGCTGCAGCCCGGGGCAGCCCTCCGGCGGCGGCTTGCCCTTCTCCCG 254

Qy     241 GCCCCGGGACTCCGGGAAGTGGGGTTCCTAGGCATGGGCCAACTTTTTTGGCGGATTGTTT 300
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Qy     301 CTTGCTTTCCAGGCTTTGCGCGTGCCAAAATCCAGTGCTACCAGTGTTGAAAGAANTTCAGCT-GA 359
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Db     315 CTTGCTTTCCAGGCTTTGCGCTGCCAAAATCCAGTGCTACCAGTGTTGAAAGAANTTCAGCTAGA 374

Qy     360 ACAACGACTGCTCCTCCCCCGAGTTCATTGTGAATTGCACGGTGAACGTTCAGACATGT 419
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     420 GTCAGAAGAAGTGATGGAGCAAAGTGCCGGGGATCATGTACGGCGGTGAACTTCATGCATCAT 479
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Db     495 CAGCGCGCCTGTCTCATCGCCTCTGCGGGGTACCAGTCCTTCTGCTCCCCAGGGAAAACTGA 554

Qy     540 ACTCAGTTTGCATCAGCTGCTGCCAACACCCCTCTTTTGTTACCGGCCCAAGGCCCAAGAAA 599
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Qy     600 GGGGAAAGTCTTGCCTCGGGCCCTCAGGCCCAGGGCTCCGCCACCACCATCTCCTGTTCCTCAAAT 659
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Db     615 GGGGAAGTTCTGCCTCGGGCCCTCAGGCCCAGGGCTCCGCCACCACCATCTGTTCCTCAAAT 674

Qy     660 TAGCCCTCTTCTCGGCACACTGCTGAAGCTGAAGGAGGATGCCACCCCTCCTGCCATTGTT 719
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Db     675 TAGCCCTCTTCTCGGCACACTGCTGAAGCTGAAGGAGGAGATGCCACCCCTCCTGCCATTGTT 734

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Qy     900 AAGGAGGTGGAGTGAAAGTTCACCCCCATGTGTCTGTGTGTAACCGGAGTCAAAGGGCAGGCTGG 959
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Qy    960  CAGAGTCWGTCCTTAGAAGTCACTGAGGTGGGCATCTGCCTTTGTAAAGCCTCCAGTGT  1019
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Qy   1140  TGAAAACCATTCTCTGCCAGCAGAAATTGGCTGGGTTTCGCGCCTGAGTTGGGCTCTAGTGAC  1199
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Qy   1200  TCGAGACTCAATGACTGGGACTTAGACTGGGGGCCTCGCGCCTCCTCTCTGAAAAGTTAAG  1259
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Db   1215  TCGAGACTCAATGACTGGGACTTAGACTGGGGGCCTCGCGCCTCCTCTCTGAAAAGTTAAG  1274

Qy   1260  AAAATCTTCTCAGTTCTCTCCTTGCCAGAGGACTCGGCGCGCGGGGACGCGAAAGAACGGGCGC  1319
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Qy   1860  AAATGCTTTAGACAGTGTA  1878
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 10:10:48 ; Search time 52.9982 Seconds
                                           (without alignments)
                                           3937.596 Million cell updates/sec

Title: US-09-970-966-214
Perfect score: 1897
Sequence: 1 gccaactccggaggctctgg...........aaaaaaaaaaaaaaaaaaa 1897

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0
Searched: 193892 seqs, 55004114 residues

Total number of hits satisfying chosen parameters: 387784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1523.2	80.3	1524	6	US-10-230-437-15	Sequence 15, Appl1
2	46	2.4	1524	6	US-10-270-333-38	Sequence 38, Appl
3	46	2.4	2196	6	US-10-270-333-37	Sequence 37, Appl1
4	45	2.4	6472	6	US-10-270-333-37	Sequence 37, Appl1
5	44.6	2.4	667	7	US-60-416-172-67	Sequence 67, Appl1
6	42	2.2	4563	6	US-10-125-923A-311	Sequence 311, Appl
7	41.8	2.2	4526	6	US-10-240-965-86	Sequence 86, Appl1
8	41.8	2.2	1734	6	US-10-230-437-155	Sequence 155, App
9	41.8	2.2	1734	6	US-10-125-923A-201	Sequence 201, Appl
10	40.8	2.2	1209	6	US-10-274-177-9	Sequence 9, Appl1
11	40.2	2.1	836	6	US-10-240-965-254	Sequence 254, App
12	40.2	2.1	3901	6	US-10-240-425-1425	Sequence 1425, Ap
13	39.8	2.1	1524	6	US-10-230-437-15	Sequence 15, Appl
14	39.2	2.1	5715	6	US-10-240-425-357	Sequence 357, App
15	39	2.1	1901	6	US-10-143-031A-18	Sequence 18, Appl
16	39	2.1	1901	6	US-10-145-092A-18	Sequence 18, Appl
17	39	2.1	1901	6	US-10-162-522A-18	Sequence 18, Appl
18	39	2.1	1901	6	US-10-165-038A-18	Sequence 18, Appl
19	39	2.1	1901	6	US-10-165-353-18	Sequence 18, Appl
20	39	2.1	1901	6	US-10-172-039A-18	Sequence 18, Appl
21	39	2.1	1901	6	US-10-172-039A-18	Sequence 18, Appl
22	39	2.1	1901	6	US-10-145-016A-18	Sequence 18, Appl
23	39	2.1	1901	6	US-10-145-088A-18	Sequence 18, Appl
24	39	2.1	1901	6	US-10-145-129A-18	Sequence 18, Appl
25	39	2.1	1901	6	US-10-125-923A-47	Sequence 47, Appl
26	39	2.1	1901	6	US-10-165-353A-18	Sequence 18, Appl
27	38.6	2.0	1032	1	PCT-US02-12342-2	Sequence 2, Appl1
28	38.6	2.0	1149	1	PCT-US02-12342-1	Sequence 1, Appl1
29	38.6	2.0	1376	1	PCT-US02-12342-4	Sequence 4, Appl1
30	38.6	2.0	8906	6	US-10-240-851-85	Sequence 85, Appl
31	38.4	2.0	610	6	US-10-264-237-199	Sequence 199, Appl
32	38.4	2.0	4098	6	US-10-240-425-1428	Sequence 1428, Ap
33	38.2	2.0	9889	6	US-10-270-333-196	Sequence 196, Appl
34	38	2.0	1251	6	US-10-270-333-98	Sequence 98, Appl1
35	38	2.0	9268	6	US-10-270-333-97	Sequence 97, Appl1
36	37.4	2.0	2954	6	US-10-240-965-82	Sequence 82, Appl1
37	37.4	2.0	4034	6	US-10-240-965-161	Sequence 161, App
38	37.4	1.9	5927	6	US-10-270-333-115	Sequence 115, App
39	36.6	1.9	3305	6	US-10-145-087A-73	Sequence 73, Appl1
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44	36.6	1.9	3305	6	US-10-165-353-73	Sequence 73, Appl1
45	36.6	1.9	3305	6	US-10-170-481A-73	Sequence 73, Appl1

ALIGNMENTS

RESULT 1
US-10-230-437-15
Sequence 15, Application US/10230437
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C94
CURRENT APPLICATION NUMBER: US/10/230,437
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/065873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 15
  LENGTH: 1524
  TYPE: DNA
  ORGANISM: Homo Sapien
US-10-230-437-15

Query Match   80.3%;   Score 1523.2;   DB 6;   Length 1524;

Best Local Similarity 99.9%; Conservative 2; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1522;

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGCTGAAGCTGAAGGAGAGTGCCACCCCCTCCTCCAGCCCTTGGCCCCCAA 600

Qy    740 CCCCCACCCCTCCGAGTGAGTTTCTTCTGGGTGTCCTTTATTCTGGGGTAGGGAGCGGG 799
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CCCCCACCTCCTGAGTGAGTTTCTTCTGGGTGTCCTTTATTCTGGGGTAGGGAGCGGG 660

Qy    800 AGTCCGTGTTCTCTTTTTGTTCCTGTGCAAATAATGAAAGAGCGTCGGTAAAGCATTCTGAA 859
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGTCCGTGTTCTCTTTTTGTTCCTGTGCAAATAATGAAAGAGCTCGGTAAAGCATTCTGAA 720

Qy    860 TAAATTCAGCYTGACTGAAATTTTCAGTTATGTACTTGAAGGAGGAGTGGGAGTGAAAGTT 919
          |||||||:||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TAAATTCAGCCTGACTGAATTTTCAGTATGTACTTGAAGGAAGGAGTGGGAGTGAAAGTT 780

Qy    920 CACCCCCATGTCTGTGTTGTAACCGGAGTCAAGGCCAGGCTGGCAGAGTCNGTCCTTAGAAGT 979
          ||||||||||||||||||||||||||||||||||||||||||||||||||:||:|||||||||
Db    781 CACCCCCATGTCTGTGTTGTAACCGGAGTCAAGGCCAGGCTGGCAGAGTCAGTCCTTAGAAGT 840

Qy    980 CACTGAGGTGGGCATCTGCCCTTTTGTTGTAAAGCCTCCAGTTTCCAATCCCTGATGGGG 1039
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CACTGAGGTGGGCATCTGCCCTTTTGTTGTAAAGCCTCCAGTTTCCAATCCCTGATGGGG 900

Qy   1040 GCATAGTTTGAGACTGCAGAGTGAGAGTGACGTTTTCTTTAGGGCTTGGAGGGCCAGTTCCC 1099
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCATAGTTTGAGACTGCAGAGTGAGAGTGACGTTTTCTTTAGGGCTTGGAGGGCCAGTTCCC 960

Qy   1100 ACTCAAGGCTCCCTCGGCTTGACATTCAGAAACTTCATGCTTGAAAAACCATTCTCTGCAGC 1159
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ACTCAAGGCTCCCTCGCGTTGACATTCAGAAACTTCATGCTTGAAAAACCATTCTCTGCAGC 1020

Qy   1160 AGAATTGGCTGGTTTCCGCGCCTCAGTTGGGCCTCTTAGTGACTCGAGACTCAATGACTGGGA 1219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AGAATTGGCTGGTTTCGCGCCCTCTGAGTTGGGCCTCTTAGTGACTCGAGACTCAATGACTGGGA 1080

Qy   1220 CTTAGACTGGGGCTCGGCCTCGGCCCTGCCGCTTCTGGAAAAGTCGCTTAAGAAAAGTCTTCTCCT 1279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CTTAGACTGGGGCTCGGCCCTGGCCCTGCCGCTTCTGGAAAAGTCGCTTAAGAAAAGTCTTCTCCT 1140

Qy   1280 TGCAGAGGAGGACTGGGCGCCGGCCGGGCCTTCCGCGGGAGAGCAAACGGCAACGGGCCGCTGTC 1339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TGCAGAGGACTGGGCGCCGGCCGGGCCTTCCGCGGGAGACCAAACGGCAACGGGCCGCTGTC 1200

Qy   1340 GGTGGTTGGAGTGCGGCATGTACGGCGGCAGGCCGGCCTTCTCGGTTGGGCGTGCCAGGACAG 1399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GGTGGTTGGAGTGCGGCATGTACGGCGGCAGGCCGGCCTTCTCGGTTGGGCGTGCCAGGACAG 1260

Qy   1400 GCGGCGACAGCACGACACCTGCACGACGACACCCCGCGCAAACTGCTGCGGACGCACCGTGTACAG 1459
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GCGGCGACAGCACGACACCTGCACGACGACACCCCGCGCAAACTGCTGCGGACGCACCGTGTACAG 1320

Qy   1460 GAGCGGGTTGATGACCGGAGCTGAGGTAGGAAAAACGTCTCCGAGAAGGGGGGAGGGGATCAT 1519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GAGCGGGTTGATGACCGGAGCTGAGGTAGGAAAAACGTCTCCGAGAAGGGGAGGGGATCAT 1380

Qy   1520 GTACGCCCCGGAAAGTAGGAACCTCGGTCCAGTGCTGCTTGGGTTTGGGGCCGCAGCCATGATCCT 1579
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GTACGCCCCGGAAAGTAGGAACCTCGTCCAGTGCTGCTTGGGTTTGGGGCCGCAGCCATGATCCT 1440

Qy   1580 CCGAATCTGGTTGGCCATCCAGCATACGGCGGCCAATCTCACAACAATCAGCCTGGGCGAGAC 1639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CCGAATCTGGTTGGCCATCCAGCATACGGCCAATCTCACAACAATCAGCCTGGGCGAGAC 1500

Qy   1640 ACGAGCAGGAGGAGGAGGGAGAGACAGAGA 1663
          ||||||||||||||||||||||||||||||
Db   1501 ACGAGCAGGAGGAGGGAGAGACAGAGA 1524
```

RESULT 2
US-10-270-333-38/c
Sequence 38, Application US/10270333
GENERAL INFORMATION:
 APPLICANT: Cravchik, Anibal
 TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
 TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES
 TITLE OF INVENTION: THEREOF AS INSECTICIDAL TARGETS
 FILE REFERENCE: CL00733CON
 CURRENT APPLICATION NUMBER: US/10/270,333
 CURRENT FILING DATE: 2002-10-15
 PRIOR APPLICATION NUMBER: 60/168,677
 PRIOR FILING DATE: 1999-12-03
 PRIOR APPLICATION NUMBER: 60/175,691
 PRIOR FILING DATE: 2000-01-12
 PRIOR APPLICATION NUMBER: 60/191,638
 PRIOR FILING DATE: 2000-03-23
 NUMBER OF SEQ ID NOS: 198
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 38
 LENGTH: 2196
 TYPE: DNA
 ORGANISM: Drosophila
US-10-270-333-38

Query Match 2.4%; Score 46; DB 6; Length 2196;
Best Local Similarity 52.6%; Pred. No. 0.019; Mismatches 90; Indels 0; Gaps 0;
Matches 100; Conservative 0;

```
Qy   1333 CGCTGTCGGTGGTTGGAGTGCGGCATGTACGGCGGCAGGCCGGCCTTCTCGGTTGGGCGTGCCA 1392
          ||| |||  |  ||||  ||||||||||||  || || ||| |  ||||| ||| ||| || ||
Db   1888 CGCTCGCCGTTGGAGTGCGGCATGTACGGCCAGGCGGACCTTCTCGGTGGTGATGTGCCGGTT 1829

Qy   1393 GCGACAGGCGGCAGCACGACACCTGCACGACACCCCGAAACTGCTGCGGACGCACCG 1452
          |||    ||  ||| | ||||| |||||||||  ||  || |  |||| ||| |||
Db   1828 GGCCCAGACAAAGTGAGCAGCCGCCCCAGAAGAACCCCTGCCGAAATTTGGAGGACATCAAGG 1769

Qy   1453 TGTACAGGAGGACGCGGTTGATGACCGAGCTGAGGTAGGAAAAACGTCTCCGAGAAGGGGAGGA 1512
          || ||||||  || ||  |  ||||| || |||| |||| ||  ||||  || ||||
Db   1769 
```

Db   1768 TGTAGAGGATCGGGTTCATGGCTGAGTTTAGGTAGAGCAATGAAGCGCGAGAAGTACAGCA 1709
          |||| ||| ||| ||| |||||||| | ||||||| | || ||| ||
Qy   1513 GGATCATGTA 1522
          ||| | |||
Db   1708 GGTTGTAGTA 1699

RESULT 3
US-10-270-333-37/c
Sequence 37, Application US/10270333
; GENERAL INFORMATION:
;   APPLICANT: Cravchik, Anibal
;   TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
;   TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES
;   TITLE OF INVENTION: THEREOF AS INSECTICIDAL TARGETS
;   FILE REFERENCE: CL0007333CON
;   CURRENT APPLICATION NUMBER: US/10/270,333
;   CURRENT FILING DATE: 2002-10-15
;   PRIOR APPLICATION NUMBER: 60/168,677
;   PRIOR FILING DATE: 1999-12-03
;   PRIOR APPLICATION NUMBER: 60/175,691
;   PRIOR FILING DATE: 2000-01-12
;   PRIOR APPLICATION NUMBER: 60/191,638
;   PRIOR FILING DATE: 2000-03-23
;   NUMBER OF SEQ ID NOS: 198
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
;   LENGTH: 6472
;   TYPE: DNA
;   ORGANISM: Drosophila
US-10-270-333-37

Query Match   2.4%;   Score 46; DB 6; Length 6472;
Best Local Similarity 52.6%;   Pred. No. 0.033;
Matches 100; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy   1333 CGCTGTCCGGTCGGAGTCCGCAATGTACGCGCAGCGCGCCGCTTCTCGTGGTTGGCGTGCTGCTGCA 1392
          | || ||| || |||||||||| || || || ||||| ||||||| |||||| |||||| |||
Db   5164 CGCCTGCCGTTGGAATGCTCCTCTGTAGTGTGGCCATGCTGGCCATGGTGGTCGCGTT 5105

Qy   1393 GCGGACAGGCGGGCAGCACCAGCACCACCTGCACGAACACCGCCGAAACTGCTCGAGGACACCG 1452
          ||||| ||| || | ||| | |||| ||| | ||| ||| |||||| ||
Db   5104 GGCCCAGACAAGTGAGCAGCAGCGCCCCAGAAGCCGCTGCGAAATTGGCAGGACATCAGGT 5045

Qy   1453 TGTACAGGAGCGGCGGTTGATGACCGAGCTGAGGTAGAAAAACGTCTCCGAGAGAGGGAGGA 1512
          |||| ||| || ||| || || |||| |||| || | | | || ||| || ||
Db   5044 TGTAGAGGATCGGGTTCATGGCTGAGTTTAGGTAGAGCAATGAAGCGCGAGAAGTACAGCA 4985

Qy   1513 GGATCATGTA 1522
          ||| | |||
Db   4984 GGTTGTAGTA 4975

RESULT 4
US-60-416-172-67
Sequence 67, Application US/6041672
; GENERAL INFORMATION:
;   APPLICANT: Cheng, Hwai Wen
;   APPLICANT: Fels, Katherine A.
;   APPLICANT: Warren, Amy J.
;   APPLICANT: Cooper, Judith R.
;   TITLE OF INVENTION: Genes from Human Cancer Cells and Human Tumors
;   FILE REFERENCE: 216019-153
;   CURRENT APPLICATION NUMBER: US/60/416,172
;   CURRENT FILING DATE: 2002-10-04
;   NUMBER OF SEQ ID NOS: 141
;   SOFTWARE: Patentin version 3.1
; SEQ ID NO 67
;   LENGTH: 667
;   TYPE: DNA
;   ORGANISM: Gallus gallus
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Human extended sequence for VOG3_71
US-60-416-172-67

Query Match   2.4%;   Score 45; DB 7; Length 667;
Best Local Similarity 46.8%;   Pred. No. 0.019;
Matches 141; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

Qy   1316 GCGCTGCACAAAGCCGGGCGCGGCCTGTCGGTGGGTGGGCCATGTACGGCGGCCGTCTC 1375
          | || | | ||| || || | || | || | || || | |||| || ||
Db   187 GCGCGAGAGCACAGCAGCGCGTACGGCGGTGGCCTGGGTGCCACGCCTTCGGAGCGGGA 246

Qy   1376 GTGGTTGGCGTGCTGGTGCCCAGCCACAGCAGCGCGGCCACGCACCACGACGACACCTCC 1435
          ||| ||||||| || || ||| ||||| || ||||| || || || || || ||||||
Db   247 GTGGGTGGAGTGCGGCACGGCGCACGGGCCAGACCCCGCCAGACCCCGCCAGACCCCGCA 306

Qy   1436 CTGCCTGCGACGACACCGTGTTACAGGAGCGGCGGGTTGATGACCGAGCTGAGGTAGAAAAACGT 1495
          ||| | ||| || || || ||| |||| ||| | || || |||| ||||| || | ||
Db   307 GTACGAGGACTTCATGGAGTGCATCACCCGACCCAGACTGGCTCTTGCGGTTGTTGAGAGAT 366

Qy   1496 CTCCGGAGAGGGGGAGGAGGATCATGTTACGCCCGGAAGTAGGACGTCGGTGGTTGAAAAAGAT 1555
          | | ||| | | || || | || | | |||| || || ||| || | | || || | ||
Db   367 CCTGGAGCAGAGGGACAAGATGATCAAGGAGGGGAAGTACACACCCCGGCGAGTACCACAA 426

Qy   1556 GGGTTTGGCGCGCAGCCCATGAACCTCCGAAATCTGGTTGGGCCATCCAGCATACGGCCAATGT 1615
          || ||| || | | || || || ||||| ||| | | ||| || | | ||| ||| |
Db   427 GGGTGAGGAAGGAACACCCGGCGCCCTGAGGCCACAGGACCTGCAGGGACCCGACACAGCGCTCGT 486

Qy   1616 C 1616
          |
Db   487 C 487

RESULT 5
US-10-125-923A-311/c
Sequence 311, Application US/1012592A3A
; GENERAL INFORMATION:
;   APPLICANT: Baker Kevin P.
;   APPLICANT: Chen, Jian
;   APPLICANT: Desnoyers, Luc
;   APPLICANT: Goddard, Audrey
;   APPLICANT: Godowski, Paul J.
;   APPLICANT: Gurney, Austin L.
;   APPLICANT: Pan, James
;   APPLICANT: Smith, Victoria
;   APPLICANT: Watanabe, Colin K.
;   APPLICANT: Wood, William I.
;   APPLICANT: Zhang, Zemin
;   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;   TITLE OF INVENTION: ACIDS ENCODING THE SAME
;   FILE REFERENCE: P3430R1C79
;   CURRENT APPLICATION NUMBER: US/10/125,923A
;   CURRENT FILING DATE: 2002-01-15
;   PRIOR APPLICATION NUMBER: 10/052586
;   PRIOR FILING DATE: 2002-01-15
;   PRIOR APPLICATION NUMBER: 60/059263
;   PRIOR FILING DATE: 1997-09-18
;   PRIOR APPLICATION NUMBER: 60/059266
;   PRIOR FILING DATE: 1997-09-18
;   PRIOR APPLICATION NUMBER: 60/062250
;   PRIOR FILING DATE: 1997-10-17
;   PRIOR APPLICATION NUMBER: 60/063120
;   PRIOR FILING DATE: 1997-10-24
;   PRIOR APPLICATION NUMBER: 60/063121
;   PRIOR FILING DATE: 1997-10-24
;   PRIOR APPLICATION NUMBER: 60/063486
;   PRIOR FILING DATE: 1997-10-21
;   PRIOR APPLICATION NUMBER: 60/063540
;   PRIOR FILING DATE: 1997-10-28
;   PRIOR APPLICATION NUMBER: 60/063541
;   PRIOR FILING DATE: 1997-10-28
;   PRIOR APPLICATION NUMBER: 60/063544
;   PRIOR FILING DATE: 1997-10-28

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 311
; LENGTH: 4563
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 3635
; OTHER INFORMATION: unknown base
US-10-125-923A-311

Query Match   2.4%; Score 44.6; DB 6; Length 4563;
Best Local Similarity   51.9%; Pred. No. 0.062;
Matches 125; Conservative   0; Mismatches 114; Indels   2; Gaps   1;

Qy   1 GCCAACTCCGGAGGCTCTGGTGTCTCGGCCCGGAGCGCGAGGGAGGACGAGAGACCCG 60
          |||| ||| | | ||| ||| ||||| |||| ||||||| | ||| ||
Db 642 GCCCGGAACCGGCAGCCCTCGGGGTGGCGCCGTGGGGCCCCCGTTCCCTTCAGCTCGG 583

Qy   61 CAGCCGGGGAGCCCGGCGGGGGGGGATGCAGGGTCCGGGCGCCACCTGCGGCTCCTCTA 120
          |||| || || |||||| |||||| |||| |||||| | |||||| |
Db 582 AAGCCCGGGGGCAGGAGACGAGCGCGGAAGCGCACGAGACGCCCGAGCAGCA 523

Qy 121 AGCTACGACGGTCGTTCTCCGGCGGGCAGCACCCCCAGCAAGCCTCGGCAGCC--ACA 178
          ||| || | | ||||| | |||| || ||| |||||||| |||
Db 522 CGCTGAGCCAGGCGGGGCGGGGCCAATGCCCGGCGTCGGCGCGGGGGC 463

Qy 179 GCCCCTGCAGCCGGCGGGGCCACCCTCGCTGCTGTCGGCGGCTTGCCCTCTCC 238
          ||| | |||| |||| ||| | | |||| ||| | |||||| |||
Db 462 GCCGCGCGCGCGGGCGGCAGCCTCGCGGGCGCCGCGGCCGCCTGCCCCGCC 403

Qy 239 C 239
          |
Db 402 C 402

RESULT 6
US-10-240-965-86
; Sequence 86, Application US/10240965
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: SHIFFMAN, Dov
; APPLICANT: SOMOGYI, Roland
; APPLICANT: LAWN, Richard M.
; APPLICANT: SEILHAMER, Jeffrey J.
; APPLICANT: PORTER, Gordon J.
; APPLICANT: MIKITA, Thomas
; APPLICANT: TAI, Julie
; TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION
; FILE REFERENCE: PA-0025 PCT
; CURRENT APPLICATION NUMBER: US/10/240,965
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 60/195,106
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PERL Program
; SEQ ID NO 86
; LENGTH: 4526
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 251776.11
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 3982, 3984-4029, 4489-4490, 4492-4493, 4495-4497, 4501-4502,
4506-4508, 4510-4512
; OTHER INFORMATION: a, t, c, g, or other
US-10-240-965-86

Query Match   2.2%; Score 42; DB 6; Length 4526;
Best Local Similarity   53.7%; Pred. No. 0.28;
Matches   87; Conservative   0; Mismatches   75; Indels   0; Gaps   0;

Qy   5 ACTCCGGAGGCTCTGGTGTCCTCGGCCCCGGAGCGCCGGAGGGGAGGACGAGAGACCCGAGC 64
          ||||||| ||| | ||| ||| | |||| || |||| ||| |||
Db 173 AGTGCTCCGGGACGGATGGTGCGGCGGGGGGGAGGGGGGGAGGAGGACCACGGCGGGCCGCGTGGAGC 232

Qy   65 CGGGAGCCCGGACGGCGGGGGGGATGCAAGGGTCGCAGGCCTCCCGGAGGGGGGGACCTGCGGGCTCTCTAAGGCT 124
          |||| ||| |||| ||||||| ||| | | |||| ||| | || ||||| ||||| |||||||||
Db 233 CGGGCGCGCCGTGCAGCCGCGAGCTGCCGCCGCCGGGGGCGCATGCGGCTGGCGCCCCGGGGCCCCTCGCG 292

Qy 125 ACGACCCGTCGTCTCCGGCGCAGCACCGGGGCCCCAGCCAGCC 166
          | |||| || ||||||| || || | |||||||| |||||
Db 293 CCCGGCCTCGGCGCCCCGGCGCCCCCAGCCCCAGCCCCAGCCC 334

RESULT 7
US-10-230-437-155/c
; Sequence 155, Application US/10230437
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C94
; CURRENT APPLICATION NUMBER: US/10/230,437
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 155
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-230-437-155

Query Match   2.2%; Score 41.8; DB 6; Length 1734;
Best Local Similarity   59.8%; Pred. No. 0.19;
Matches   70; Conservative   0; Mismatches   47; Indels   0; Gaps   0;

Qy 114 TCCTCTAAGCTACGACCGTCGTCTCCGGCGCAGCACCGGGGCCCCAGCCAGCCTCGGCAG 173
          | | | | || | || | || ||| | || | | | || || | | |
Db 1091 TCACCTCTGTCTGCCACCACATTGTTGCCACTGCTCGCTGCTCGCCGGCCACTGCTGCCG 1032

Qy 174 CCACAGCCCGCTGCAGCCGGGGCAGCCTCCGGCGCCTCCGTGCTGTCGCGCCTCCTGTCGATCGCGTTG 230
          |||| ||| | || ||| || | ||| || || || | || || || | | ||| ||| |||
Db 174 TCACCTCTGTCTGCCACCACATTGTTGCCACTGCTCGCTGCTCGCCGGCCACTGCTGCCG 230

```
Db  1031  CCACTGCTGCTGCCACTGCTGCTGCCACCACTGCTGCTGCCATTG  975
```

RESULT 8
US-10-125-923A-201/c
Sequence 201, Application US/10125923A
GENERAL INFORMATION:
;   APPLICANT: Baker,Kevin P.
;   APPLICANT: Chen,Jian
;   APPLICANT: Desnoyers,Luc
;   APPLICANT: Goddard,Audrey
;   APPLICANT: Godowski,Paul J.
;   APPLICANT: Gurney,Austin L.
;   APPLICANT: Pan,James
;   APPLICANT: Smith,Victoria
;   APPLICANT: Watanabe,Colin K.
;   APPLICANT: Wood,William I.
;   APPLICANT: Zhang,Zemin
;   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;   TITLE OF INVENTION: ACIDS ENCODING THE SAME
;   FILE REFERENCE: P3430R1C79
;   CURRENT APPLICATION NUMBER: US/10,125,923A
;   CURRENT FILING DATE: 2002-01-15
;   PRIOR APPLICATION NUMBER: 10/052586
;   PRIOR FILING DATE: 2002-01-15
;   PRIOR APPLICATION NUMBER: 60/059263
;   PRIOR FILING DATE: 2002-01-15
;   PRIOR APPLICATION NUMBER: 60/059266
;   PRIOR FILING DATE: 1997-09-18
;   PRIOR APPLICATION NUMBER: 60/062250
;   PRIOR FILING DATE: 1997-09-18
;   PRIOR APPLICATION NUMBER: 60/063121
;   PRIOR FILING DATE: 1997-10-24
;   PRIOR APPLICATION NUMBER: 60/063120
;   PRIOR FILING DATE: 1997-10-24
;   PRIOR APPLICATION NUMBER: 60/063540
;   PRIOR FILING DATE: 1997-10-28
;   PRIOR APPLICATION NUMBER: 60/063541
;   PRIOR FILING DATE: 1997-10-28
;   PRIOR APPLICATION NUMBER: 60/063544
;   PRIOR FILING DATE: 1997-10-28
;   PRIOR APPLICATION NUMBER: 60/063486
;   PRIOR FILING DATE: 1997-10-21
;   PRIOR APPLICATION NUMBER: 60/063185
;   PRIOR FILING DATE: 1997-10-17
;   PRIOR APPLICATION NUMBER: 60/059263
;   PRIOR FILING DATE: 1997-09-18
;   Remaining Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 612
;   SEQ ID NO 201
;   LENGTH: 1734
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-125-923A-201

Query Match   2.2%; Score 41.8; DB 6; Length 1734;
Best Local Similarity 59.8%; Pred. No. 0.19; Matches 70; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

```
Qy  114  TCCTCTAAGCTACGACCGTCGTCCGCGGCAGCAGCGGCGGCCCAGCCAGCCTCGGCAG  173
         ||| ||  |   |   ||  |  |   |   | |   | |||   |  ||  ||||  |||
Db  1091 TCACCTCTGCCACCATGTTGCCACTGCTGCCACTGCTGCCACTGCTGCCG  1032

Qy  174  CCACAGCCGCGTGCAGCCGGGGCAGCCTCCGCGTGTTCGCCTCTCTGAtGGCCTTG  230
         ||  | |||  |||||| ||||||||  || |
Db  1031 CCACTGCTGCCACTGCTGCCACCACTGCTGCTGCCACTGCTGCCATTG  975
```

RESULT 9
US-10-274-177-9/c
Sequence 9, Application US/10274177
GENERAL INFORMATION:
;   APPLICANT: MARKOWITZ, Sanford D.
;   TITLE OF INVENTION: METHODS FOR CATEGORIZING PATIENTS
;   FILE REFERENCE: CWRU-P01-003
;   CURRENT APPLICATION NUMBER: US/10/274,177
;   CURRENT FILING DATE: 2002-10-18
;   PRIOR APPLICATION NUMBER: US/10/229,345
;   PRIOR FILING DATE: 2002-08-26
;   NUMBER OF SEQ ID NOS: 20
;   SOFTWARE: Patentin version 3.1
;   SEQ ID NO 9
;   LENGTH: 1209
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1161)..(1161)
;   OTHER INFORMATION: n=a, c, g, or t
US-10-274-177-9

Query Match   2.2%; Score 40.8; DB 6; Length 1209;
Best Local Similarity 50.0%; Pred. No. 0.29; Mismatches 127; Indels 1; Gaps 1;
Matches 128; Conservative 0;

```
Qy  27   GCCCGGGAGCGGCGAGCCGGGGAGGAGGAGAGAGAACCCGAGCCCGGGAGCCCGGAGCCCGGGGGGGAT  86
         ||||||   ||  |   || | |   | |||| || |  ||  ||||||  ||  | ||||   |  |  |
Db  412  GCCCCGCCCCGCCGAGTCGGCCCATGGCAGCCGGATGAGCCGCGAGTACGAGTRAGGGGGGCT  353

Qy  87   GCAGGCTCCGCGAGCGGGCACCTGCGGCTCTTCTTACCGAACCGTGTCTCCGCGCGCAG  146
         ||  |  | |   ||  |  ||     |    |   |||   || | |    ||  | |
Db  352  TGGGCCGCCGCCGTATATATGGGTGTTGCTGCGTGCAGCACCCTCGCCGCCTCCCCGCGCCCCGCC  293

Qy  147  CAGCCGCGGGGCCCCAGCCAGCCTCGGCGAGACCACAGCCGCGCTGCAGCCGCGGGGGCAGCCTCCGCTG  206
         ||| |   |    ||  ||  || |  | |   |     |   | |  | |||  | | |||  | || |
Db  292  CTGGCCCCGCCGCCCCCGGCCTTCCGCGCCCCTCGCGCCACCACCGCTGCACTTCGTTCGCCGTCGCCG  233

Qy  207  CTGTCGCCCTCCTCTCGATGCGGCTTGCCCCTCCCCGGGGACTTCCGGAGAATGTGGG  266
         || | |||| ||| | |||  ||  |||| | |||  ||||   |||| || | | |
Db  232  GGATCGGCCTCCTCCGC-GCCCGGCCCGCCGCCGCCGCGCACTCTGTTCGCCGTCGCCCCTTGCGTA  174

Qy  267  TCCTTAGGCAtCGCGGC  282
         | |  |||| |||| ||
Db  173  TCTCTGGGCGCGCCGC  158
```

RESULT 10
US-10-240-965-254
Sequence 254, Application US/10240965
GENERAL INFORMATION:
;   APPLICANT: INCYTE GENOMICS, INC.
;   APPLICANT: SHIFFMAN, Dov
;   APPLICANT: SOMOGYI, Roland
;   APPLICANT: LAWN, Richard M.
;   APPLICANT: SEILHAMER, Jeffrey J.
;   APPLICANT: PORTER, Gordon J.
;   APPLICANT: MIKITA, Thomas
;   APPLICANT: TAI, Julie
;   TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION
;   FILE REFERENCE: PA-0025 PCT
;   CURRENT APPLICATION NUMBER: US/10/240,965
;   CURRENT FILING DATE: 2002-10-04
;   PRIOR APPLICATION NUMBER: 60/195,106
;   PRIOR FILING DATE: 2000-04-05
;   NUMBER OF SEQ ID NOS: 276
;   SOFTWARE: PERL Program
;   SEQ ID NO 254
;   LENGTH: 836
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 243574.11
US-10-240-965-254

Query Match   2.1%; Score 40.2; DB 6; Length 836;
Best Local Similarity 50.3%; Pred. No. 0.34; Mismatches 98; Indels 0; Gaps 0;
Matches 99; Conservative 0;

```
Qy  15   CTCTGGTGCTCGGCCCGGGAGGCGGGAGGCGGGAGCCGGAGCGGGAGGGGGAGGAGCAGAGAGACCCGACGCGGGGAGCCCG  74
```

```
Db   38 CTTGGCCCTTGGGCCTTAGATTCGAGGTCTCCCAGGGTCCCAAGTCCTGGGTTCAGAGGGCGG
         |||   |||  ||||  |||  |||  ||||  |||  |||||| |||   |||  |||  ||
Qy   75 AGCGCGGGGCGGATGCAGCGTCCGCGAGCGGCCACCTGCCGCTCCCTCTAAGCTACGACCGTCG 134
         ||||  |||  |||  |||  ||||  |||  |||  |||  |||  |||||  |||  |||
Db   98 GGGCGGAGGGGCGGTGTCTCCAAGGGGGGTCCCGGGGTCCCTGAAAGGCGCGGGACCA 157
         ||||  |||  |||  |||||  |||  |||  |||  ||||||  |||  |||
Qy  135 TCTCCGCGGCGAGCACGCGGGGCCCCAGCACCTCGGCAGCCACACCCGCTGCAGCCGCGGG 194
         |||  |||  |||  ||||||  |||||  |||  |||  ||||||  |||  |||
Db  158 GGGCGGGATCACCCAGTCTCGCGCCGCTGCAGCCCCCGTGCCGCCCACCCGTGCCGCCGCA 217
         |||  |||||||  |||  |||  ||||||  |||  |||||||  |||  |||
Qy  195 CAGCCTCCGCTGCTGTC 211
         ||||||  |||  |||
Db  218 CCGGACCCGGAGCCCC 234
```

RESULT 11
US-10-240-425-1425/c
Sequence 1425, Application US/10240425
GENERAL INFORMATION:
;   APPLICANT: Williams, Amanda
;   APPLICANT: Boland, Joseph F.
;   APPLICANT: Lord, Reginald V.
;   APPLICANT: Alvarez, Chris
;   APPLICANT: Wetzel, Jon C.
;   APPLICANT: Scherf, Uwe
;   APPLICANT: Vockley, Joseph G.
;   TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
;   FILE REFERENCE: 44921-5026
;   CURRENT APPLICATION NUMBER: US/10,240,425
;   CURRENT FILING DATE: 2002-09-30
;   PRIOR APPLICATION NUMBER: PCT/US01/09847
;   PRIOR FILING DATE: 2001-03-28
;   PRIOR APPLICATION NUMBER: US 60/193,446
;   PRIOR FILING DATE: 2000-03-31
;   NUMBER OF SEQ ID NOS: 1588
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1425
;   LENGTH: 3901
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. U25997
US-10-240-425-1425

Query Match   2.1%; Score 40.2; DB 6; Length 3901;
Best Local Similarity 57.6%; Pred. No. 0.74;
Matches   72; Conservative   0; Mismatches   53; Indels   0; Gaps   0;

```
Qy  138 CCGGCGGCGAGCAGGCGGGGGCCCAGCACCAGCAGCCGTTCGGCCAGCAGCCGGGGGGGAG 197
         ||| ||||||||||| || || ||| | ||| ||  || ||||| ||| ||| || ||
Db  125 CTGCTGCTGCCACCGGTGCCTCCGCCTCGCTGCTCGTCGCCGGCGCCGTCGCCGTCGCTG 66
Qy  198 CCTTCCGCTGTCGTCGCCTTCCTCTGATTCGCGCTTGCCCTCTCGTCTGCCCGCGGCGTCGTGCGGGGACTCCGGGA 257
         ||||| || | ||||| || || || | || ||  || |||||| ||  || |||  || ||
Db   65 CCACCGCCGCGCTCGCTGCCAGTCGCTGCTTCGTCTTCGCACCTCTGGCTTTTTCCA 6
```

```
Qy  258 GAATG 262
         | ||
Db    5 AACTG 1
```

RESULT 12
US-10-230-437-15/c
Sequence 15, Application US/10230437
GENERAL INFORMATION:
;   APPLICANT: Baker, Kevin P.
;   APPLICANT: Desnoyers, Luc
;   APPLICANT: Gerritsen, Mary
;   APPLICANT: Goddard, Audrey
;   APPLICANT: Godowski, Paul J.
;   APPLICANT: Grimaldi, J. Christopher
;   APPLICANT: Gurney, Austin L.

;   APPLICANT: Smith, Victoria
;   APPLICANT: Stephan, Jean-Philippe F.
;   APPLICANT: Watanabe, Colin L.
;   APPLICANT: Wood, William I.
;   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;   TITLE OF INVENTION: ACIDS ENCODING THE SAME
;   FILE REFERENCE: P3530P1C94
;   CURRENT APPLICATION NUMBER: US/10,230,437
;   CURRENT FILING DATE: 2002-08-28
;   PRIOR APPLICATION NUMBER: 10/119,480
;   PRIOR FILING DATE: 2002-04-09
;   PRIOR APPLICATION NUMBER: 60/059113
;   PRIOR FILING DATE: 1997-09-17
;   PRIOR APPLICATION NUMBER: 60/062287
;   PRIOR FILING DATE: 1997-10-17
;   PRIOR APPLICATION NUMBER: 60/063549
;   PRIOR FILING DATE: 1997-10-28
;   PRIOR APPLICATION NUMBER: 60/064103
;   PRIOR FILING DATE: 1997-10-31
;   PRIOR APPLICATION NUMBER: 60/069873
;   PRIOR FILING DATE: 1997-12-17
;   PRIOR APPLICATION NUMBER: 60/078910
;   PRIOR FILING DATE: 1998-03-20
;   PRIOR APPLICATION NUMBER: 60/079294
;   PRIOR FILING DATE: 1998-03-25
;   PRIOR APPLICATION NUMBER: 60/079656
;   PRIOR FILING DATE: 1998-03-26
;   PRIOR APPLICATION NUMBER: 60/079728
;   PRIOR FILING DATE: 1998-03-27
;   PRIOR APPLICATION NUMBER: 60/079728
;   PRIOR FILING DATE: 1998-03-27
;   Remaining Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 15
;   LENGTH: 1524
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-230-437-15

Query Match   2.1%; Score 39.8; DB 6; Length 1524;
Best Local Similarity 67.5%; Pred. No. 0.58;
Matches   56; Conservative   0; Mismatches   27; Indels   0; Gaps   0;

```
Qy  143 GCAGCACGCGCGGGGCCCCAGCAGCCTCGGCCAGCCACAGCCGCTGCAGCCGGGGGGCAGCCTCC 202
         || | ||| ||||| ||| ||||| |||| | ||| || ||| ||||| || ||||||| ||
Db   86 GCATCAGAGGAGGGCGACAGCAGCAGCGGGGAGGCTCCCCCGGCTGCAGCGGCGCCTGGTGCCCGGCTGGGGCTGGGCCGCGAG 27
Qy  203 GCTGCTGTGTCGCCTCCTTCTGATGC 225
         |||||||  |  |  |   | || ||
Db   26 GCTGCTGGGGGGCCGCGCGCTGCTGC 4
```

RESULT 13
US-10-240-425-357
Sequence 357, Application US/10240425
GENERAL INFORMATION:
;   APPLICANT: Williams, Amanda
;   APPLICANT: Boland, Joseph F.
;   APPLICANT: Lord, Reginald V.
;   APPLICANT: Alvarez, Chris
;   APPLICANT: Wetzel, Jon C.
;   APPLICANT: Scherf, Uwe
;   APPLICANT: Vockley, Joseph G.
;   TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
;   FILE REFERENCE: 44921-5026
;   CURRENT APPLICATION NUMBER: US/10,240,425
;   CURRENT FILING DATE: 2002-09-30
;   PRIOR APPLICATION NUMBER: PCT/US01/09847
;   PRIOR FILING DATE: 2001-03-28
;   PRIOR APPLICATION NUMBER: US 60/193,446
;   PRIOR FILING DATE: 2000-03-31
;   NUMBER OF SEQ ID NOS: 1588
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 357
;   LENGTH: 5715

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AB023157
US-10-240-425-357

Query Match
Best Local Similarity   2.1%;   Score 39.2; DB 6; Length 5715;
Matches 80; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

```
Qy  100 GCGGCACCTGCGGCTTCTAAGCTACGACCGTCGTTCCGGCGCAGCAGCCGCGGGCCCC 159
            |||||| |   |||   |||| | |||  ||||||| | | |||||| ||||| |||
Db  532 GAGGCACTTTCTCCCCCAGATCGGCCTTGGCCGCGAGACCCACGCACCACCAGCCGC 591

Qy  160 AGCAGCCTTCGGCACCACCAGCCGCCTGCAGCCCGGGGGCAGCCTTCGGCGGTCCGCTCC 219
            ||| || |||  || | ||||||||||| || || ||||||| || ||| | | |||
Db  592 CGCCTGCGCCCCCCGCCCCCAGCCGCCGGCACACCAGCCAGCCACCACCAGGCGCCGCC 651

Qy  220 TGATGCGCTTGCCCTCTCCCGGGCCCGG 247
            |   |  | ||| || | ||||| |||
Db  652 AGCAGCGCGCGCTCACCCGCCCAGCCCCAG 679
```

RESULT 14
US-10-145-087A-18
; Sequence 18, Application US/10145087A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C47
; CURRENT APPLICATION NUMBER: US/10/145,087A
; CURRENT FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 624
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SEQ ID NO 18
; LENGTH: 1901
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-145-087A-18

Query Match
Best Local Similarity   2.1%;   Score 39; DB 6; Length 1901;
Matches 92; Conservative 0; Mismatches 70; Indels 1; Gaps 1;

```
Qy   57 CCCCAGCCGCGGGGAGCCCGACGCGCGGCGGGCGGATGCAGCCTTCCCGCGGAGCGGCGTCC 116
            |||| ||  || | |||  || | | ||||| | || |||||| || ||| |||  ||
Db    9 CCCGGCGGCCGGCGCCCGCCGAAGCCGGGAGCCACCGGCCATGGGGGGGCCTGCCTGGGAGGCCTGC 68

Qy  117 TCTAAGCTACGACCGTCGTCTCCGGCGGCAGCAGCGGGGCCCCAGCAGCCTTCGGCGGTCCGCTCC 176
            ||| | |   | | || ||| | ||| | |||| | ||  ||||| || |||  ||| |||||
Db   69 TCCTGGCTCAGCTCGGCGTC-CTGCCTCCTCGCGGCTTCTGCCCCTGCCCGCCCCTGCATTCCTGTGCAGCTG 127

Qy  177 CAGCCGCGTCGCAGCCGCGGGGGGCAGCCTCCGGCTGCTGGCTCCCCTC 219
            ||| |   | | |  | ||| ||| | ||  || || |||| |||
Db  128 CTGCCCCGCCCAGCCCAACTCCACCGTGAGCGCGCTCATCTTC 170
```

RESULT 15
US-10-143-031A-18
; Sequence 18, Application US/10143031A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C39
; CURRENT APPLICATION NUMBER: US/10/143,031A
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03

```
;   PRIOR APPLICATION NUMBER: 60/065311
;   PRIOR FILING DATE: 1997-11-13
;   PRIOR APPLICATION NUMBER: 60/066364
;   PRIOR FILING DATE: 1997-11-21
;   PRIOR APPLICATION NUMBER: 60/077450
;   PRIOR FILING DATE: 1998-03-10
;   PRIOR APPLICATION NUMBER: 60/077632
;   PRIOR FILING DATE: 1998-03-11
;   PRIOR APPLICATION NUMBER: 60/077641
;   PRIOR FILING DATE: 1998-03-11
;   PRIOR APPLICATION NUMBER: 60/077649
;   PRIOR FILING DATE: 1998-03-11
;   PRIOR APPLICATION NUMBER: 60/077791
;   PRIOR FILING DATE: 1998-03-12
;   Remaining Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 624
;   SEQ ID NO 18
;     LENGTH: 1901
;     TYPE: DNA
;     ORGANISM: Homo sapiens
US-10-143-031A-18

Query Match           2.1%;    Score 39;   DB 6;   Length 1901;
Best Local Similarity   56.4%;   Pred. No. 1;
Matches     92; Conservative   0; Mismatches    70; Indels    1; Gaps   1;

Qy     57 CCCGCAGCCGGGAGCCCGAGCGCGGGGGGCGGATGCAGGCTCCGGAGCGGGCACCTGCGGCTCC 116
          ||||  ||||  ||| | || ||  | | | ||||| | || |  | |  || ||  | | |
Db      9 CCCGGCGCCGGGCGCCCGAAGCCGGGAGCCACCCCCATGGGGGCCTGCCTGGGGAGCCTGC   68

Qy    117 TCTAAGCTACGACCGTCGTTCTCCGCGGAGCAGCAGCGCGGGCCCCAGCAGCCTTCGGCAGCCA 176
          || ||| |  |  |||||   |  | | | |  | || | ||| |  ||| |  ||||  ||||
Db     69 TCCCTGCTCAGCTGCGCGGTC-CTGCCCTCTTGCGGCGGCTTCGCCCCCTTGCCATCCTGTGCCAGCTG 127

Qy    177 CAGCGCGCTGCAGCCGGGGGGGCAGCCTCCGCTGCTGTCGGCCTCCTC 219
          |  ||| |||||||  | ||| |  |||| | |  |  | | | | || ||
Db    128 CTGCCCCGGCCCAGCGCCAACTCCACCGTGAGCCGCCTCATCTTC 170

Search completed: November 7, 2002, 18:02:24
Job time : 85.9982 secs
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OM nucleic - nucleic search, using sw model

                                    GenCore version 5.1.3
                                    Copyright (c) 1993 - 2002 Compugen Ltd.

Run on:              November 7, 2002, 09:52:52 ; Search time 2541.39 Seconds
                                    (without alignments)
                                    12088.985 Million cell updates/sec

Title:               US-09-970-966-214
Perfect score:       1897
Sequence:            1 gccaactccggaggctctgg..........aaaaaaaaaaaaaaaaa 1897
Scoring table:       IDENTITY_NUC
                     Gapop 10.0 , Gapext 1.0
Searched:            16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters:          32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     EST:*
          1:   em_estba:*
          2:   em_esthum:*
          3:   em_estin:*
          4:   em_estmu:*
          5:   em_estov:*
          6:   em_estpl:*
          7:   em_estro:*
          8:   em_htc:*
          9:   em_estl:*
         10:   gb_est2:*
         11:   gb_htc:*
         12:   gb_est3:*
         13:   gb_est4:*
         14:   gb_est5:*
         15:   em_estfun:*
         16:   em_estom:*
         17:   gb_gss:*
         18:   em_gss_hum:*
         19:   em_gss_inv:*
         20:   em_gss_pln:*
         21:   em_gss_vrt:*
         22:   em_gss_fun:*
         23:   em_gss_mam:*
         24:   em_gss_mus:*
         25:   em_gss_other:*
         26:   em_gss_pro:*
         27:   em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES

Result                  %     Query
 NO.   Score  Match  Length  DB ID         Description
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c  1    798   42.1    888     14  BQ689771   BQ689771 AGENCOURT
c  2    764.8  40.3   814      9  AI567376   AI567376 AL567376
c  3    741.2  39.1   920      9  AL538562   AL538562 AL538562
c  4    709.2  37.4   987     14  BQ668420   BQ668420 AGENCOURT
c  5    700.8  36.9   821     12  BG752229   BG752229 602731372
c  6    698.8  36.8   702     14  BQ005545   BQ005545 UI-H-EI1-
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c   7  678.8  35.8  1490  11  AK012406  AK012406 Mus muscu
c   8  672.4  35.4   678   9  AI936826  AI936826 wp699h10.x
c   9  672.4  35.4   696  13  BM547680  BM547680 AGENCOURT
c  10  664.2  35.0   747  13  BI917149  BI917149 603181571
c  11  658.8  34.7   799  11  BE271770  BE271770 601141674
c  12  657.6  34.7   676  10  BE385990  BE385990 601276636
c  13  651.4  34.3   704  13  BI919074  BI919074 603180881
c  14  651.4  34.3   690  13  AW149665  AW149665 xf40h05.x
c  15  645    34.0   698  13  BI554034  BI554034 603235426
c  16  635    33.5   707  13  BI913989  BI913989 603180565
c  17  630.4  33.2   690  13  BI669845  BI669845 603180565
c  18  626.4  33.0   649  10  AW590950  AW590950 hg51e12.x
c  19  624.4  32.9   627  13  BM669397  BM669397 UI-E-DW1-
c  20  611.2  32.2   616   9  AI990500  AI990500 ws40d07.x
c  21  610.4  32.2   696  12  BF439382  BF439382 nab63g06.
c  22  609.2  32.1   850  12  BE736301  BE736301 601307087
c  23  608.2  32.1   645  12  BF432379  BF432379 nac53g11.
c  24  605.8  31.9   704  13  BI823714  BI823714 603040833
c  25  602    31.7   743  10  BF395797  BF395797 601110028
c  26  599.4  31.6   879  14  BQ689033  BQ689033 AGENCOURT
c  27  591.2  31.2   654  12  BE746601  BE746601 601580186
c  28  589    31.0   843  12  BF125134  BF125134 601762356
c  29  587.4  31.0   591  10  AI846686  AI846686 wl83d00.x
c  30  577.4  30.4   759  12  BI126050  BI126050 601762888
c  31  569    30.0   948  14  BQ882838  BQ882838 AGENCOURT
c  32  566.4  29.9  1010  12  AI742092  AI742092 wg38h03.x
c  33  560.4  29.5   578   9  BF345141  BF345141 602018318
c  34  558.8  29.5   699  10  BE395581  BE395581 60130973B
c  35  555.4  29.3   571  14  BM709964  BM709964 UI-E-CQ1-
c  36  550.8  29.0   670  12  BG753617  BG753617 602732803
c  37  549.4  29.0   551  12  BE858216  BE858216 7g19g07.x
c  38  538.4  28.4   540  12  BF939693  BF939693 nac00b12.
c  39  537    28.3   537  12  BF594242  BF594242 7n10d03.x
c  40  533.8  28.1   538  13  BM667957  BM667957 UI-E-DW0-
c  41  532.2  28.1   537   9  AI018769  AI018769 ov32e04.x
c  42  530.8  28.0   534  10  BE350014  BE350014 ht07g12.x
c  43  530.8  28.0   561  10  AW150789  AW150789 xg39c02.x
c  44  526.8  27.8   589  10  AI859538  AI859538 wm13c03.x
c  45  525.4  27.7   527  10  AW338938  AW338938 ha68h04.x
```

```
                              ALIGNMENTS

RESULT 1
BQ689771
LOCUS        BQ689771                 888 bp    mRNA    linear    EST 15-JUL-2002
DEFINITION   AGENCOURT_8344092 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6248684
             5', mRNA sequence.
ACCESSION    BQ689771
VERSION      BQ689771.1  GI:21815087
KEYWORDS     EST.
SOURCE       human.
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 888)
  AUTHORS    NIH-MGC http://mgc.ncbi.nih.gov/.
  TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL    Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM2388  row: o  column: 21
             High quality sequence stop: 665.
FEATURES             Location/Qualifiers
     source          1..888
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#12

(Left column)

```
Qy   1629 CCTGGGGCAGCACGAGCA-GGAGGGAGGAGGAGAAAGAGAAAAACACAG-CATGAGAAC 1686
          ||||| ||||||||||| | |||||||||||||||  ||||||||||    |||||||
Db    781 CCTGGGCAGCACGAGCACCAGGAGGAGGAGGAGAGAAGAGAAAAAACCCGGCCTTGGGAAC 840

Qy   1687 ACAGTAAATGAA---TAAAACCATAAAATATTTAGCCCCTCGTTCT 1730
          ||||||||||||   ||||||| |||||||| ||| |||||| |||
Db    841 ACAGTAAATGAATTAAAACCGATAAAATATATTTTAAACCCCTCTTGT 887
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RESULT 2

```
LOCUS       AL567376                 814 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL567376 LTI_FL013_FBrn1 Homo sapiens cDNA clone CS0DF024YO04 3
            prime, mRNA sequence.
ACCESSION   AL567376
VERSION     AL567376.1  GI:12920672
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 814)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr; Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1..814
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DF024YO04"
                     /clone_lib="LTI_FL013_FBrn1"
                     /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
                     cDNA was primed with a NotI-oligo(dT) primer. Five prime
                     end enriched, double-stranded cDNA was digested with Not I
                     and cloned into the Not I and Eco RV sites of the
                     pCMVSPORT 6 vector. Contact : Feng Liang Life
                     Technologies, a division of Invitrogen 9800 Medical
                     Center Drive Rockville, Maryland 20850, USA Fax : (1) 301
                     610 8371 Email ; fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
                     /dev_stage="pooled tissue from post conception fetuses (20
                     week, 24 week and 26 week)"
                     /lab_host="DH10B"
BASE COUNT  161 a  228 c  210 g  205 t  10 others
ORIGIN
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(Right column)

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Query Match      40.3%;  Score 764.8;  DB 9;  Length 814;
Best Local Similarity  97.4%;  Pred. No. 6.4e-128;
Matches  788;  Conservative  7;  Mismatches  12;  Indels  2;  Gaps  2;

Qy    915 AAGTTCACCCCCATGTCTGTGTAACCGGAGTGTCAAGGCCAGGCTGGCAGAGTCWGTCCTTA 974
          || |||| ||||||||||||||||||  ||| |||||||||||||||||||||||| ||||||
Db    809 AAAGTCMCCCCCATGTCTGTGTAACC-GAGTCAAGGCCAGGCTGGCAGAGTCAGTCCTTA 751

Qy    975 GAAGTCACTGAGGTGGGCATCTGCCTTTTGTAAAGCCTCAGTGTCCATTCCAT-CCCTG 1033
          |||||||||||||||||| ||||||||||||||||||||||||||||||||| |||||
Db    750 GAAGTCACTGAGGTGGGCAATCTGCCTTTTGTAAAGCCTCAGTGTCCATTCCATYCCCTG 691

Qy   1034 ATGGGGGCATAGTTTGAGACTGCAGAGTGAGAGTGAGCGTTTTCTTAGGGCTGGAGGGCCA 1093
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    690 ATGGGGGCATAGTTTGAGACTGCAGAGTGAGAGTGAGCGTTTTCTTAGGGCTGGAGGGCCA 631

Qy   1094 GTTCCCACTCAAGGCTCCCCTGCGTTGACATTCAAACTTCAATGCTCCTGAAAACCAATTCTC 1153
          ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db    630 GTTCCCACTCAAGGCTCCCCTGCGTTGACATTCAAACTTCATGCTCCTGAAAACCAATTCTC 571

Qy   1154 TGCAGCAGAATTGGCTGTGTTTCGCGCCCTGAGTTGGGCTCTTAGTGACTCGAGACTCAATGA 1213
          |||||||||||||  ||||||||||||||||||||  |  |||||||||||||||||||| |
Db    630 ...
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(Left column — continued)

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BASE COUNT  217 a  219 c  264 g  187 t  1 others
ORIGIN

Query Match      42.18;  Score 798;  DB 14;  Length 888;
Best Local Similarity  96.5%;  Pred. No. 6.7e-134;
Matches  856;  Conservative  2;  Mismatches  23;  Indels  6;  Gaps  4;
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Qy    850 GCAATTCTGAATAAATTCAGCYTGACTGAAATTTCACTGATGTGTACTTGAAGGAAGGAGGTGG 909
          |||||||||| ||| ||||||| |||||||||||||| || ||| || |||||||||||||||
Db      1 GCAATTCTGAAATAATTCAGCCTGACTGAAATTTCAGTATGTTCAGTAGTGTGAAGGAAGGAGGTGG 60

Qy    910 AGTGAAAGTTCACCCCCATGYTCTGTGTGTAACCGGAGTGTCAAGGCCAGGCTGGCAGAGTCWGT 969
          |||||||||||||||||||| ||||||||||||| ||||||||||||||||||||||||||  ||
Db     61 AGTGAAAGTTCACCCCCATGYTCTGTGTGTAACCCGGAGTGTCAAGGCCAGGCTGGCAGAGTCAGT 120

Qy    970 CCTTAGGAAGTCACTGAGGTGGGCATGGGCCATCTGCCTTTTGTAAAGCCTCCAGTGTCCATTCCATC 1029
          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||| |||
Db    121 CCTTAGGAAGTCACTGAGGTGGGCATGGGCCATCTGCCTTTTGTAAAGCCTCCAGTGTCCATC 180

Qy   1030 CCTGATGGGGGGCCATAGTTTGAGACTGCAGAGTGAGAGTGAGCGTTTTGTTGTTCTTAGGGCTGGAGG 1089
          ||||||||||| |||||||||||||||| ||||||||||||||||||| || ||||||||||||||||
Db    181 CCTGATGGGGGCATAGTTTGAGACTGAGAGTGAGAGTGAGCGTTTTCTTAGGGCTGGAGG 240

Qy   1090 GCCAGTTCCCACTCAAGGCTCCCCTGCGCTTGACATTCAAACTTCATGCTCCTGAAAACCAT 1149
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GCCAGTTCCCACTCAAGGCTCCCCTGCGCTTGACATTCAAACTTCATGCTCCTGAAAACCAT 300

Qy   1150 TCTCTCGCAGCAGAATTGGCTGTTCGCGCCGTTGGGCTCTTAGTGACTCGAGACTCA 1209
          ||||| ||||||||||||||||||| ||||| ||||||| | |||||||||||||||
Db    301 TCTCTGCAGCAGAATTGGCTGTTCCCGCCTGAGTTGGGCTGTCTAGTGACTCGAGACTCA 360

Qy   1210 ATGAGGACTTAGACTGGGGGGCTCGGGCCTCGGCCTCTCGAAAAGGTGGGCTTAAGAAAATCTTCT 1269
          ||||| ||||||||||||||| ||||||||||||||||||||||| | ||||||||||||||||
Db    361 ATGAGCGGGACTTAGACTGGGGGGGCTCGGGCCTCGGCCTCTCGAAAAGTGCTTAAGAAAATCTTCT 420

Qy   1270 CAGTTCTCCTTGCAGAGAGGACTGGCGCGCGGAGAGCAGCAACGCGGCGCGCTGCCAAAGC 1329
          |||||||| |||||||| ||||||||||||||||||||||||||||||||||||| |||||
Db    421 CAGTTCTTCCTTGCAGAGGACTGGCGCGCGGAGAGCAGCAACGCGGCGCGCTGCACAAAGC 480

Qy   1330 GGGCGGCTGTCGGTGGTGGAGTGCGCGCGGTACCGGCACGCGGCGCGCGCTTCTCGTTGGCGTGCT 1389
          |||||  ||||||||||||||| ||| ||||||| || |  | |||||| |||||||||| ||||||
Db    481 GGGCGCTGTCGGTGGTGGAGTGGGCGGTACCGCCGCTTCTCGTTGGTGGCGTGCT 540

Qy   1390 GCAGCGACAGGCGGCGGGCGCAGCCGGACCGGCTTGCTGCGACGCA 1449
          |||||||||||||||||||||||||||||||||||||||||||| ||
Db    541 GCAGCGACAGGCGGCGGGCGCAGCCGGACCGGCTTGCTGCGACGGACA 600

Qy   1450 CCGTGTTACAGGAGGAGCGCGGGGTTGATGACCAGTGAGAAAAACGTGTCCGGAAAGGGGA 1509
          |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db    601 CCGTGTTACAGGAGGAGCGCGGGGGGTTGATGACCAGTGAGAAAAACGTGTCCGGAAAGGGGA 660

Qy   1510 GGAGGATCATGTACGCCCGGAAGTAGGAGTAGGACCTCGTCCAGTCGT-GCTTGGGGTTTGGGCCGCA 1568
          ||||||||||||||||||||||||||||  |||||||||||||||||| |||||||||||||||| ||
Db    661 GGAGGATCATGTACGCCCGGAAGTAGGACCTCGTCCAGTCGTTGGGGTTTGGGCCCA 720

Qy   1569 GCCATGATCCTCCGAAYCTGGTTGGGGGATCCAAATGTCAACAAATCAGC 1628
          |||||||||||||||| |  | | ||||||||| | |  ||||||||||||||
Db    721 GCCATGATCCTCCGAANTCGGNTNGGGGCATCCAGCATACGGGGCAAATGTCAACAAATCAGC 780
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LOCUS   AL538562   920 bp   mRNA   linear   EST 16-FEB-2001
DEFINITION AL538562 LTI_FL013_FBrn1 Homo sapiens cDNA clone CS0DF024Y004 5
            prime, mRNA sequence.
ACCESSION   AL538562
VERSION   AL538562.1 GI:12866967
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 920)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT   Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
            Technologies. Contact : Feng Liang Life Technologies, a
            division of Invitrogen 9800 Medical Center Drive Rockville,
            Maryland 20850, USA Fax : (1) 301 610 8371 Email :
            fliang@lifetech.com URL :
            http://fulllength.invitrogen.com"
FEATURES   Location/Qualifiers
     source   1..920
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                     /db_xref="taxon:9606"
                     /clone="CS0DF024Y004"
                     /clone_lib="LTI_FL013_FBrn1"
                     /dev_stage="pooled tissue from post conception fetuses (20
                     week, 24 week and 26 week)"
                     /lab_host="DH10B"
                     /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
                     cDNA was primed with a NotI-oligo(dT) primer. Five prime
                     end enriched, double-stranded cDNA was digested with Not I
                     and Eco RV sites of the
                     pCMVSPORT 6 vector. Library was constructed by Life

RESULT 3
AL538562
AL538562

BASE COUNT   172 a   285 c   257 g   199 t   7 others
ORIGIN

Query Match   39.1%;   Score 741.2;   DB 9;   Length 920;
Best Local Similarity 94.3%;   Pred. No. 1.1e-123;
Matches 862; Conservative 4; Mismatches 36; Indels 12; Gaps 9;

Qy   4 AACTCCGGAGGCGGCTTCGGTGCTTCGGGACCGGACCGGCGA-GCGGGAGGAGGAGACCCGCA   62
           |||:||||||||||||:||||||||||||||||||||||| | ||||||||||||||||||||
Db   1 AACTCCGGAGGCGGC-GGTTGCTTCNGGACCGGGAGGCGGGAGACCGGAGGNGGGNAGGAGGACAGAGAGACCCCCA   59

Qy   63 GCCGGGAGCCCGAGCGCCGGGGGA-TGCAGGCGTCCGGGAGAGGCGGGAGGGGAAACTGAA   121
           |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db   60 GCCGGGGAGCCCGGAGANTCCAGGGTTCCGGGAGGGGGAGGGGTTCCGGGAGGGGGGGTTCCTCTAA   119

Qy   122 GCTACGGACCGTGCGTCTCCGCGGCGCAGCAGCGGG-GCCCCAGCAGCCTCGGGCAGCCCACAGC   180
           ||||||||||||||||||:|||||||||||||||||| ||||||||||||||||||||||||||
Db   120 GCTACGGACCGTCGTCTCCGCGGCGCAGCAGCGGNGCCCAGCAGGCCTCGGGCAGCCACAGC   179

Qy   181 CGCTGCAGCCGCGGGGAGAGCCCTCCGGTCTGTCGGGTGCCGGGCCCTTGCCCTTCCCG   240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   180 CGCTGCAGCCGCGGGGAGAGCCCTCCGGTCTGTCGGGTGCCGGGCCCTTGCCCTTCCCG   239

Qy   241 GCCCCGGGACTCCCGGGGAAGTGCCGGGGCATCGGGCCGCCACCTTTTTTGGGGATTGGTT   300
           |||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db   240 GCCCCGGGACTCCCGGGGANTGCCGGGGCATCGGGCCGCCACCTTGGGGATTGTT   299

Qy   301 CTTGCTTCCCAGGCTTTGCCGCTGCAAATCCAGTGCCTACCAGTGTGCAAGAATTCCAGCTGA   360
           ||||||||:|:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db   300 CTTGCTTCCCAGGCTTTGCCGCTGCAAATCCAGTGCTACCAGTGTTCAAGAATTCCAGCTGAA   359

Qy   361 CAACGACTGCTCCTCCCCGGAGTTCATTGTGAATTGCACGGTGAAGTTCAAGACAGTG   420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   360 CAACGACTGCTCCTCCCCGGAGTTCATTGTGAATTGCACGGTGAAGTTCAAGACAGTG   419

Qy   421 TCAGNAAGAAGTGATGGAGCAAAAGTGCCGGGGATCATCGTACCGCCAAGTGCCTGTGCATCATC   480
           |||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db   420 TCAGAAAGAAGTGATGGAGCAAAAGTGCCGGGGATCANGTACCGCCAAGTTCCTGTGCATCATC   479

Qy   481 AGCGCGGCCCGTGTCTCATCGCCCTCTGCGGGGTACCAGTCCTTCTCCCCAGGGAAACTGAA   540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   480 AGCGCGGCCCTGTCTCATCGCCCTCTGCGGGGTACCAGTCCTTCTCCCCAGGGAAACTGAA   539

Qy   541 CTCAGTTTGCATCAGCTGGTGCAACCCCTCTTTGTTAACGGAGGGCCCAAGAAAG   600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   540 CTCAGTTTGCATCAGCTGCTGCGAACACCCCTCTTTGTTAACGGAGGGCCCAAGAAAG   599

Qy   601 GGGAAGTTCTGCCTCGGGCCCTCAGGCCCCAGGGCCTCGCCACCATCCTGTTCCTCAAATT   660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   600 GGGAAGTTCTGCCTCGGCCCCTCAGG-CAGGGCCTCGGCCACCATCCTGTTCCTCAAATT   658

Qy   661 AGCCCTCTTCTCTCGGCCACACTGCTGAAGCTGAAGGAGGAGGATGCCACCCCCTCCTGCATTGTTTC   720
           ||||||:|:||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db   659 AGCCCTCTTCTCGCCACACTGCTGAAGCTGAAGGAGGATGCBAHCCCCTCCTGCATTGTTTC   718

Qy   721 TTCCAGCCCCTTGCCCCCAACCCCCCACCCTCCCTGAGTGAGTTTCTTCTGGGTGTCCTTTTT   780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||:|| ||||
Db   719 TTCCAGCCCCTTGCCCCCAACCCCCCACCCTCCCTGAGTGAGTTTCTTCTGGGTGT-CTTTTT   777

Qy   781 ATTCTGGGTTAGGAGCCGGAGTCCGTGTTCTCGTTTGTTCCTGTGCAAATAATAGAAAGAG   840
           |||||||||||||||||||||| |||||||||||||||||||||||||||-||||
Db   778 ATTCTGGGTTAGGAGCGCGG--AGTGCGTGTTCTTTTTGTTCCTGTGCAAATGAAAGAGCT   835

Qy   841 CTCGGTAAAGCATTCTGAATAAAATTCAGCYTGACTGAATTTTCAGTAGYACTTGAAGGA   900
           ||||||||||||||||||||||||||||||:|||||||||-||||||||||||||||||
Db   836 C---GGTAAGCAATTCTGAAT-AATTCAGCCTGACTGAATTCAGTAGYATGTACTGAAGGAGGR   891

Qy   901 AGGAGGTGGAGTGA   914

Db   570 TGCAGCAGAATTGGCTGGTTGTTCNCCCCTGAGTTGGGCTCTPAATAACTCGAGACTCAATNA   511
            |||||||||||||||||||||||| |||||:|||||||||||||||||||||||||||||
Qy   1214 CTGGGACTTAGACTGGGGCGGGCTCGTCTGAAAAGTCTTAGAAAANTCTTCTCAGT   1273

Db   510 CTGGGACTTAGACTNGGGCGGGCTCGGCCTGTCTTGAAAAGTTCTTAARAAATCTTTCAGT   451
            |||||||||||||:|||||||||||||||||||||||||||||:|||||||||||||||
Qy   1274 TCTCCTTGCAGAGGACTNGCCGCGCCGGGAAGGGCCGTGCACAAAGCGGGGC   1333

Db   450 TCTCCTTGCAGAGAACTGCCCGGGGACCGGAGACGCAACGGGCNCTGCACAAAGCGGGC   391
            |||||||||||||||||||||||||||||||:|||||||||||||||||||||||
Qy   1334 GCTGTCGGTGGTGGGGAGGTGCCCATGTACCGCCGCCGCCTTCTCGTGGTGTGGGTGGTGGGTGCCCAG   1393

Db   390 GCTGTCGGTGGTGGGGAGGTGCGCCATGTACGGCCGCCAGGCGCTTCTCGTGGTTGGCGGTGCCAG   331
            |||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||
Qy   1394 CGACAGGGGCAGCACAGCAGCGCACNCCGGCCGAAACTGCTGCCGAGGACACCGT   1453

Db   330 CSACAGGCGGGGCAGCAGCACACCTGCACGAGGACACCGGCGAAACTGCTGCGGGAGGAGACACGGT   271
            |:|||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||
Qy   1454 GTACAGGAGCGGGGTTGATGAGCAGTGAGGTAGAAAAAACGTTCTCCGAGAAGGGGAGGAG   1513

Db   270 GTACAGGAGCGGGGTTGATGACGGTGAGGTAGAAAAAACGTCTCAGCAGGGGAGGAG   211
            ||||||||||||||||||||||:|||||||||||||||||||||||||||||||||
Qy   1514 GATCATGTTACGCCCCGGGAAGTAGGAACCTCGTTCAGTGTCGTGGGTTTGGGCCCGGCAGCCAT   1573

Db   210 GATCATGTTACGCCCGGGAAGTAGGACCTCGTTCCAGTCGTGCTTTGGGTTTGGGCGTCCGTCGCAG   151
            |||||||||||||:|||||||||||:|||||||||:|||||:||||||||||||||||:|||:|||
Qy   1574 GATCCTCCGAATCTGGTTGGGCATCNCGGCGCGAATGTCACACAAATCAGCCCGTGG   1633

Db   150 GATCCTCCAAAATCTGGTTGGGCATCAACCTGCCGTGCTTCCAGTCGTGCTTGGGTTTCGCCCCG   91
            ||||||||:||||||||||||||||||:|||||||:||||||||||||||||||||||||:||:
Qy   1634 GCAGACACGAGCAGGAGGGGAGAGAGAGAAAAACGCATGAGAAACACAGTAA   1693

Db   90 GCAACACGAGCAGGAGGGGAGGGGTTGATGACCGACTGAGGTAGAAAAAAACACADCGAGAACACAGTA   31
            ||:||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Qy   1694 ATGAATAAAAACCATAAAAATATTTAGCCCC   1722

Db   30 ATGAAWAAAAACCATAAAAATATTTAGCCCC   2

```
Db    892 GTGGAGTGAAGTCA 905
          |||  |||  ||
```

RESULT 4
BQ668420

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LOCUS       BQ668420               987 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8301981 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6275121
            5', mRNA sequence.
ACCESSION   BQ668420
VERSION     BQ668420.1  GI:21778667
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 987)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2457 row: m column: 10
            High quality sequence stop: 583.
FEATURES             Location/Qualifiers
     source          1..987
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6275121"
                     /clone_lib="NIH_MGC_102"
                     /tissue_type="epidermoid carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGACGAG(G). Library constructed
                     by Ling Hong in the laboratory of Gerald M. Rubin
                     (University of California, Berkeley) using ZAP-cDNA
                     synthesis kit (Stratagene) and Superscript II RT (Life
                     Technologies). Note: this is a NIH_MGC Library."
BASE COUNT      196 a    314 c    285 g    191 t      1 others
ORIGIN
```

```
Query Match             37.4%;  Score 709.2;  DB 14;  Length 987;
  Best Local Similarity   94.2%;  Pred. No. 6.1e-118;
  Matches   758;  Conservative    0;  Mismatches   44;  Indels    3;  Gaps    2;

Qy     19 GGTGCTCGGCCCGGGGGGGAGGGAGGCAGAGAGCACCCAGCCCGGGGAGCGAGCG 78
          ||||||||||||| ||| | | || | ||||||||||||| |||||||| ||||| |
Db     11 GGTGCTCGGCCCCGGGAGCGCGAGCGGGAGGGAGGCAGAGACCCCAGCCCGAGCCCGGACCG 70

Qy     79 CGGGGCGATGCAGGCTCCGGCGACCGGCACCGGCGCCTCCTCTAAGCTACGACCGTCGTCTC 138
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     71 CGGGGCGATGCAGGCTCCGGCGACCGGCACCGGCGCCTCCTCTAAGCTACGACCGTCGTCTC 130

Qy    139 CGCGGGCAGCAGGCGGCGGGCGGGCGCCCCAGCAGCCTCGGCAGCCTGCAGCCGGGGGCAGC 198
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 CGCGGGCAGCAGGCGGCGGGCGGGCGCCCCAGCAGCCTCGGCAGCCTGCAGCCGGGGGCAGC 190

Qy    199 CTCCGCTGCTGTGTGCCGGGGGGCTTCCTTCCCCCTTCCCCGGGGACTCCGGGAG 258
          ||||||||||||||||||| | || ||||||||||||||||||||||||||||||
Db    191 CTCCGCTGCTGTGTGCCGCGGCGCTTCCTTCCCCCTTCCCCGGGGACTCCGGGAG 250

Qy    259 AATGTGTGGGGTCCTAGGCATCGCGCCGCACACTTTTTTCGCGGATTGTTGTTTCTTGCTTCC 318
          ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    251 AATGTGTGGGGTCCTAGGCATCGCGCCGCAACTTTTTTCGCGGATTGTTGTTTCTTGCTTCC 310
```

```
Qy    319 GCTGCAAATCCAGTGACTGCTACCAGTGTGAAGAACGTTGTCAGAAGAAGTGATGA 378
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Db    311 GCTGCAAATCCAGTGACTGCTACCAGTGTGAAGAACGTTGTCAGAAGAAGTGATGGA 370

Qy    379 CGAGTTCAATTGTTGAATTGCACGGTGAACGTTCAAGACACATGTGTTCAGAACATGGA 438
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Db    371 CGAGTTCAATTGTGAATTGCACGGTGAACGTTCAAGACACATGTGTTCAGAACATGGA 430

Qy    439 GCAAAGTGCCGGGATCATGTACCGGCAGCAGTCCTCTTGCATCATCAGCGGCCTCTTCATTGCC 498
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Db    431 GCAAAGTGCCGGGATCATGTACCGGCAGCAGTCCTCTTGCATCATCAGCGGCCTCTTCATTGCC 490

Qy    499 CTCTGCCGGGGTACCAGTCGTTTCGTCTCCCCAGGGAAAACTGAACTCAGTTTGCATCAGCTG 558
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Db    491 CTCTGCCGGGGTACCAGTCGTTTCGTCTCCCCAGGGAAAACTGAACTCAGTTTGCATCAGCTG 550

Qy    559 CTGCAACACCCCTCTTTTGTAACGGGCCAAGGCCCAAGAGAAAAGGGGAAGTTCGCCTCGGC 618
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Db    551 CTGCAACACCCCTCTTTTGTAACGGGCCAAGGCCCAAGAGAAAAGGGGAGTTCGCCTCGGC 610

Qy    619 CCTCAGCGCCAGGGGCTCCCCACCAACCATCCTGTTCCTCAAATTTAGCCCTCTTCTTGGCACA 678
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Db    611 CCTCAGCGCCAGGGGCTCCCGACCAACCATCCTGTTCCTCAAATTTAGCCCTCTTCTTGGCACA 670

Qy    679 CTGCCTGAAGCTGAAGGAGATGCCAACCACCACCCCCTCCCATTGTTC-TTCCAGCCCTGCCCCC 737
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Db    671 CTGCCTGAAGCTGAAAGAGATGCCAACCACCCCCTCCCATTGGTCTTTCCACCCCTGCCCCC 730

Qy    738 AA--CCCCCACCTCCCTGAGTGAGTTTCTTCTGGGTGTCCTTTTATTCTGGGTAGGGAG 795
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Db    731 AAACCCCCCACCTTCCCTGAGTGGAGTTCCTTCTCGGGGTGGCCCTTTTAATTCCTGGGTT 790

Qy    796 CGGGAGTCCGTGTGTTCTCTTTTTGTTC 820
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Db    791 AAGGAGCCGGGAAACCCCGGGGTTC 815
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RESULT 5
BG752229

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LOCUS       BG752229               821 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602731372F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4875113 5',
            mRNA sequence.
ACCESSION   BG752229
VERSION     BG752229.1  GI:14062882
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 821)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1755 row: o column: 18
            High quality sequence stop: 770.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /tissue_type="normal pigmented retinal epithelium"
                     /lab_host="DH10B (phage-resistant)"
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RESULT 6

/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"

BASE COUNT   194 a   201 c   248 g   178 t
ORIGIN

Query Match   36.9%; Score 700.8; DB 12; Length 821;
Best Local Similarity 95.5%; Pred. No. 2.1e-116;
Matches 785; Conservative 2; Mismatches 24; Indels 11; Gaps 6;

Qy   834 GAAAGAGCTCGGTAAAAGCATTCTGAATAAAATTCAGCYTGACTGAATTTTCAGTAYGTACT 893
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Db   2 GAAAGAGCTCGGTAAAAGCATTCTGAATAAAATTCAGCCTGACTGAATTTTCAGTATGTACT 61

Qy   894 TGAAGGAAGGAGGTGGAGTGAAAGTTCACCCCCATGTCTGTGTACCGGAGTCAAGGCCA 953
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Db   62 TGAAGGAAGGAGGTGGAGTGAAAGTTCACCCCCATGTCTGTGTACCGGAGTCAAGGCCA 121

Qy   954 GGCTGGCAGAGTCWGTCCTTAGAGTCACTGAGGTGGGCATCGTGCCTTTTGCCTTTTGTAAAGCCTC 1013
         ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   122 GGCTGGCAGAGTCAGTCCTTAGAGTCACTGAGGTGGGCATCGTGCCTTTTGCCTTTTGTAAAGCCTC 181

Qy 1014 CAGTGTCCATTCCATNCCCTGATGGGGGCAATAGTTTGAGACGTGCAGAGTGAGAGTGACGTT 1073
         |||||||||||||| |||||||||||||| ||||||||||| ||||||||||||||||||||
Db   182 CAGTGTCCATTCCATCCCTGATGGGGGCATAGTTTGAGACTGCAGAGTGAGAGTGACGTT 241

Qy 1074 TTCTTAGGGCTGGAGGGCCAGTTCCCACTCAAGGCTCCCTCGCTTGACATTCAAACTTCA 1133
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Db   242 TTCTTAGGGCTGGAGGGCCAGTTCCCACTCAAGGCTCCCTCGCTTGACATTCAAACTTCA 301

Qy 1134 TCGTCCTCGAAAACCATTCTCTCGCAGCAGAATTGGCTGGTTCGCGGTTGGGCTCT 1193
         ||||||||||||| |||| |||||| ||||||||||||||||||| |||||||||
Db   302 TGCTCCTCGAAAACCATTCTCTCGCAGCAGAATTGGCTGGTTCGCGCCTGAGTTGGGCTCT 361

Qy 1194 AGTGACTCGAGACTCAA----TGACTGGGACTTAGACTGGGGCCTCGGCCTCGCTCTCT---G 1246
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Db   362 AGTGACTCGAGAATCCAATTGAATTGGGAACTTAAACGGGGCGCCGCCTCGGCCTCGCTCTCTAG 421

Qy 1247 AAAAGTGCTTAAGAA--AATCTTCTCAGTTCTCCTTGCCAGAGGACGGGGGACGGCGGA 1305
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Db   422 AAAAGTGCTTAAGAATAATCTTCTCAGTTCTCCTTGCAGAGGACGGGGGACGGCGGA 481

Qy 1306 AGAGCAACACGGGGCGCGCTGCACAAAACGGGGGCCCTGTGTCCGTGGAGTCGCCATGTACCGCCA 1365
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Db   482 AGAGCAACGGGGGCGCGCTGCACAAAACGGGGGCCCTGTGTCCGTGGAGTCGCCATGTACCGCA 541

Qy 1366 GGGCCTTCTCGTGGTTGGGCGTTGCGTCAGCGACAGCGCCAGCACCGCACG--AAC 1424
         |||||| |||||||||||||| |||||||| |||||||||| ||||||||| |||
Db   542 GCGGCTTCTCGTGGTTGGGCGTTGCGTCAGCGACAGCGCCAGCACCGCACCTGCACGAAAC 601

Qy 1425 ACCGGCCGAAACTGCTGCGAGGACACCGTGTACAGGAGCAGCCGGTTGATGACCGAGCTGAGG 1485
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Db   602 ACCGGCGAAACTGCTGCGAGGACACCGTGTACAGGAGCGGTTGATGACCGAGCTGAGG 661

Qy 1485 TAGAAAAACGTCTCCGAGAAAGGGGAGGAGGATCATGTACGGCCCGGAAGTAGGACCTCGTC 1544
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Db   662 TAGAAAAACGTCTCCGAGAAAGGGGAGGAGGATCATGTACGGCCCGGAAGTAGGACCTCGTC 721

Qy 1545 CAGTGTCGTTCCTTGGGGTTTGGGCGGCAGCCATGATCTCCGAAATCTGGTTGGGCCATTCCAGACAT 1604
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Db   722 CAGTGTCGTTCCTTGGGGTTTGGGCGGCAGCCATGATCTCCGAAATCTGGTTGGGC-TTCAGCAT 780

Qy 1605 ACGGCCAATGTCACAACAATCAGCCCTGGGCGAGACACGAGCA 1646
         |||||||||||||||||||||||||||||||||||||||||||
Db   781 ACGGCCAATGTCACAACAATCAGGCCT-GGCAGAGACACGAGCA 821

BQ0006545/c

BASE COUNT   137 a   200 c   163 g   202 t
ORIGIN

Query Match   36.8%; Score 698.8; DB 14; Length 702;
Best Local Similarity 99.7%; Pred. No. 5e-116;
Matches 700; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1194 AGTGACTCGAGGACTCAATGACTGGGGACTTAGACTGGGGCCTCGGCCTCGCTCTCTGAAAAGTG 1253
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   702 AGTGACTCGAGGACTCAATGACTGGGGACTTAGACTGGGGCCTCGGCCTCGCTCTCTGAAAAGTG 643

Qy 1254 CTTAAGAAAATCTTCTCAGTTCTCCTTGCAGAGGACTGGCGCCGGGGACGGCGGAAGAGCAAC 1313
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Db   642 CTTAAGAAAATCTTCTCAGTTCTCCTTGCAGAGGACTGGCGCCGGGGACGGCGGAAGAGCAAC 583

Qy 1314 GGGCGCTGCACAAAAGCGGGGGCCCTGTGTCCGTGGAGTCGCCATGTACCGCCAGCGGCTTC 1373
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Db   582 GGGCGCTGCACAAAAGCGGGGGCCCTGTGTCCGTGGAGTCGCCATGTACCGCCAGCGGCTTC 523

Qy 1374 TCGTGGTTGGGCGTTGCGTCAGCGACAGCGCCAGCACCGCACGAACACCGGCCGA 1433
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RESULT 7

AK012406

```
Qy    522  TCGTGGTTGGCGGTTCTGCAGCGACGAGGCGGCGCAGCACCTCCACGACACCCGCCGA  463
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Db   1434  AACTGCTCGCGAGAGACACCGTGTACAGGAGGAGCGGGGTTGATGAGCCGAGCTGAGGTGAGAAAAC  1493

Qy    462  AACTGCTCGCGAGAGACACCGTGTACAGGAGGAGGAGACCACCCGTGCTGAGGCTGAGGTGAGAAAAC  403

Qy   1494  GTCTCCGAGAAGGGAGAGGGGAGGATCAGTGTACGCCCCGGAAGTAGGACTTCGTCCACTCGTGTCC  1553
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Db    402  GTCTCCGAGAAGGGAGAGGGGAGGATCAGTGTACGCCCCGGAAGTAGGACCTCGTCCAGTCGTGC  343

Qy   1554  TTGGGTTTGGCCCGCAGCCATGATCCTCCCGGAATCTCGGTTTGGGACTTCCAGCATACGGCCAAT  1613
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Db    342  TTGGGTTTGGCCCGCAGCCATGATCCTCCCGGAATCTCGGTTTGGGGACTTCCAGCATACGGCCAAT  283

Qy   1614  GTCACACAACAATCAGCCCTGGGCAGCACACGAGGGAGAGGGAGGAGGGAGGAAAAGAAAAC  1673
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Db    282  GTCACACAACAATCAGCCCTGGGCAGCACACGAGGGAGAGGGAGGAGGGAGAGGAAAAAAAAAC  223

Qy   1674  ACAGCATGAGACACAGTAAATGAATAAAAACCATAAAAATATTTAGCCCCTCGTTCTGTG  1733
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Db    222  ACAGCATGAGAGACACAGTAAATGAATAAAAACATAAAAATATTTAGCCCCTCGTTCTGTCTG  163

Qy   1734  CTTACTGGCCAGGAAATGGTACCAATTTTTTCAGTGTTGTGGACTTGACACAGCTTCTTTTTTGCCA  1793
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Db    162  CTTACTGGCCAGGAAATGGTACCAATTTTTTCAGTGTTGTGGACTTGACACAGCTTCTTTTTTGCCA  103

Qy   1794  CAAGCAAGAGAGAATTTAACACTGTTTCAAAACCCGGGGAGTTGGCGTCGTGTTAAAGAAAG  1853
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Db    102  CAAGCAAGAGAGAATTTAACACTGTTTCAAAACCCGGGGAGTTGGCTGTGTTAAAGAAAG  43

Qy   1854  ACCATTAAATGCTTTAGACAGTGTAAAAAAAAAAAAAAAAAAAA  1895
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Db     42  ACCATTAAATGCTTTAGACAGTGTAAAAAAAAAAA  1
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LOCUS   AK012406   1490 bp   mRNA   linear   HTC 19-JAN-2002
DEFINITION Mus musculus 11 days embryo whole body cDNA, RIKEN full-length
            enriched library, clone:2700050C12:BRAIN cDNA, CLONE MNCB-0671,
            full insert sequence.
ACCESSION   AK012406
VERSION   AK012406.1 GI:12849129
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (strain:C57BL/6J) 11 days embryo cDNA to mRNA,
            clone.lib:RIKEN full-length enriched mouse cDNA library
            clone:2700050C12.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE   High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99272253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsunto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,M., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE   RIKEN integrated sequence analysis (RISA) system-384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
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            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
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            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
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            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C.A., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE   Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
   PUBMED   11217851
REFERENCE   5 (bases 1 to 1490)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
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            Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
            Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,
            Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
            Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
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            Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE   Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp;
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)

COMMENT   Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. Second
            strand cDNA was prepared with the primer adapter of sequence [5'
            GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCC 3'], cDNA was cleaved
            with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
            Host: SOLR.

FEATURES   Location/Qualifiers
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                     /strain="C57BL/6J"
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                     /clone="2700050C12"

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CDS
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        /dev_stage="11 days embryo"
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        /translation="MLQSOAAAEHLPEHLPELLRGHVVEERVDHRAEVEESIREGQED
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        K"
```

```
BASE COUNT      366 a    370 c    405 g    349 t
ORIGIN
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Query Match   35.8%;   Score 678.8; DB 11;   Length 1490;
Best Local Similarity   71.1%;   Pred. No. 1.6e-112;
Matches 1023; Conservative 2; Mismatches 369;   Indels   44; Gaps   8;

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Qy    311 GGCTTTGCGCTGCAAATCCACTGCTACCAGTGTGAGAGAAATTCCACTGACAACGACTGC 370
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Db     64 GGGCTGGGCGGCCTGCAAATTCAGTGCTCACCAGTGTGAGAGAAATTCCAGTGACAACTGC 123

Qy    371 TCCTCCCCCGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATTGTGTCAGAAAGAA 430
          ||| | |||| |||||||| ||||||||| |||||| ||||| |||||| |||||||| ||
Db    124 TCATCCCCTGAGTTCATCGTGAAATTGCACCGTGAACGTTCAAGACATGTGTCAGAAAGAA 183

Qy    431 GTGATGGAGCAAAAGTGCCGGGATCCATGAGTACCGCAAGTCCGTGTGCAATCATCAGCGG 490
          || ||||||||||||||||| ||||| ||| |||||| ||||| |||||| || |||||||
Db    184 GTGATGGAGCAAAAGTGCTGGGATCATGAGTACCGGAAGTCGTGTGTCGTGATCAGCGGT 243

Qy    491 CTCATCGGCTCTCCGGGGTACCACTCCTTGTCCCCGGAAAACTGACACTCAGTTTGC 550
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Db    244 CTCATTGCTTCAGCTGGGTACCAGTCCTTCTTGTCCCCGGGAAAACTGACTCCGTGTGC 303

Qy    551 ATCAGCTGCTGCAACACCCCCTCTTTTGTTAACGGCGCCAAGCCCAAGAAAAAGGGGAGTTCT 610
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Db    304 ATCAGCTGCTGCAACACCCTCTTTGCAATGGCGCCAACGCCCAAGAAGACGACCAGCTCT 363

Qy    611 GCCTCCGCGCCCTCAGGCACGGGCTCCGCAGCCACCACATCCTGTTCCTCCAAATTAGCCC 670
          ||||| ||||| |||||| || |||||||| || |||||| ||||||| |||| |||||||
Db    364 GCCTCGGCCATCAGGCAGGCTTCACCACTCTTCCTGTCTCCACTTAGCCCTCTGC 423

Qy    671 TCGGCACACTGCTGAAGGTGAAGGAGATGCCACCCCTCCTGCATTGTTCTTCCAGCCCCT 730
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Db    424 TTGGCACACTGCTGAAGCTAAAGGAGAGTGCCAACCCCTGCTCCTCACCTGTCTCGGCCCT 483

Qy    731 CGCCCCCAACCCCCGAGTGAGTTTTCTTCTGGGTGTCCTTTTATTCTGGGTA 790
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Db    484 TCGTCTCTCACCTTCCC------GAGTCTCTTGGGTGTCCTTTTATTCTGGGTA 533

Qy    791 GGGAGCGGGAGTCCGTGTGTTCTTTGGTTGTTCGTTGCAAATAA------TGAAAGAGCTC 843
          |||| | |||||||||| ||| ||||||| ||||||||||| ||      |||||||||||
Db    534 GACAAGGGAGTCTTTTGTTCCTCTTTCAAGTAACGCAAGATTGCCCGTGCACAAAATAC 593

Qy    844 GGTAAAGACATTCGAATAAAATTCAGCYTGACTGAATTTCA------GTATGTACTTGAAG 898
          ||| |||| |||| ||||||| ||||| || |||||||||||      ||||| |||||||
Db    594 TTTTGTAAGCTCGAACCAAATTCATTCTGAATTTCGTGAGTTGATGTTGAAGAAAAGCAT 653

Qy    899 GAAGGAGGTGGGAGTGAAAGTTCACCCCCATGTCTGTGTGTAACCGAGTCAAGGCCAGGCTG 958
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Db    654 GGAGCAGAAAGTCCAGACCTCCAAATCTGGTTAACCACCGCCAAGGCTAGCCTG 713

Qy    959 GCAGAGTCWGTCCTTACAAGTCACTGAGGTGGGCCATCTGGATGGGGGGGGGCCATAGT 1018
          ||| ||| | ||||||||||||||||||||||| ||||||||| ||||||||| ||| |||
Db    714 GAAGAACCAG--CCTTAGGAGTCATTGAGATACCGCATCTGCCTTTCCCAAAGCCTTGAGCT 772

Qy   1019 TCCATCCATCCCCTGAGGGGGGGGCCAT------------TTGAGACTGCAGAGTGAGAGT 1067
          |||| |||| |||| ||| ||||||||||            || |||| || ||| |||||
Db    773 TCCAATCTGTGCCCAGTAGGAGTCACACTCTTATTCAGAGACTGCTGCTCCGTGAAGGTAAC 832

Qy   1068 GACGTTTTCTTAGGCGTCGGAGGGCCCAGTCCCACTCAGGGCTCCTCCGCTTGACATTCAA 1127
          || |||||| || | | |||||||||||||||||||||||| |||| |||||||||||||||
Db   1068 GACGTTTTCTTAGGCGTGGGAGGGCCCAGTCCCACTCAGGGCTCCTCCGCTTGACATTCAA 1127
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RESULT 8
AI936826/c
LOCUS   AI936826   678 bp   mRNA   linear   EST 08-MAR-2000
DEFINITION   wp69h10.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2467075 3'
             similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
             GPR39. ;, mRNA sequence.
ACCESSION   AI936826
VERSION   AI936826.1   GI:5675696
KEYWORDS   EST.
SOURCE   human.
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 678)
  AUTHORS   NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE   National Cancer Institute / National Institute of Neurological
             Disorders and Stroke, Brain Tumor Genome Anatomy Project
             (CGAP/BTGAP), Tumor Gene Index
  JOURNAL   Unpublished (1998)
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgaps-r@mail.nih.gov
             Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
             Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
             Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:

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Db    833 TTTGCTTTGCGGGAGGGGAGGAGAGCCAGTTTCGGCTCAAGGCTTCTGAACTTGCCATTCAT 892

Qy   1128 ACTTCAATGCTCCTGAAAACCATTCTCTGCAGCAGAAGAATTGGCTGGGTTCGGCCGAGTTG 1187
          |  |||||| || |||| || || || |||||| || |||||| |||||| |||| |||||
Db    893 ACTTCCTGCTCCTGTATAAACTATTTTCTGGGGTGGGACCCAGCTGGTTGGTCTCTGAGCCA 952

Qy   1188 GGCTCTAGTGACTCGGAGGACTCAAATGACTGGGAGTTAGACT--GGGGTCGGCCCTGCGTC 1244
          |||||||||||||||| |||||| ||  ||| | |||| ||||   ||||| ||||| ||||
Db    953 GTCTGTGGGTGACTCAGGAGCTCAAAGGGCTTAGGCTTCCAGGCTTGGCCCTTGCGTC 1012

Qy   1245 TGAAAAGTGCTTAAGAAAAATCTTCTCAGTTCTCCTTCCAGAGGACT------GGCGCCGG 1298
          || ||||| ||||||| ||||||| || ||| |||| || ||||| |      ||| ||||
Db   1013 TGAAAAGTGCTTAAGAAAAACCTTGTTAGTTCTTCCTGGAGGAGAGTTACTGCGCCGGGAG 1072

Qy   1299 GACGCGGAAAGGAGCCAAGGGGCGGCCTGCACAAAGGCCCGCTCGGTGGTGGTGGGCATGT 1358
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Db   1073 GCTAGGAGAGGAGGGGCCTGCGGGGCTGAGCTGGTGCTGTTCCTTGGGTGGAGGATGAAGCGG 1132

Qy   1359 ACGCGCAGGGCGCTTCTCCGTGGTTGGGGTTTTGGGGCCGGCCGACACAGCCAGCACCTGC 1418
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Db   1133 GCACCGTGGGGTTTCTCTCGTGGTGTGCATCGTGCAGAGTCAGCGGCAGCAGACGCACCTGC 1192

Qy   1419 ACGAACACCCCGCGAAAACTGCTGCGAGAACACACCGTGTACAGAGGAGGCGGGGTTGAG 1478
          | |||| |||| ||||||||| || ||||||| |||||||| |||||| || ||| ||
Db   1193 CAGAACACCTTCCGGAACTGCCTAGGACCACAGTTGTAGAGAGGAGGGTTGACCACAGAG 1252

Qy   1479 CTGAGGTAGAGAAAAACGTCTCCGAGAAGGGAGGGGGGAGGATCATGTACGCCCCGGGAAGT 1538
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Db   1253 CTGAGGTAGAGAAAGGTATCAGAGAGGGGATCAATGTATGCCCTGAAGTTACGTT 1312

Qy   1539 CTCGTCCCAGTGCTGCTTGGGTTTGGGGCCGGCCAGCCATGAATCCTCCGGAATCTGGTTG 1598
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Db   1313 CTGGTACAGTCATGTTTGGGTTTTTTGGTGGCTGCGACCACCATGATCCTCGGAGTCTGATTGGGGATC 1372

Qy   1599 CAGCATACGGCCAATGTCACAACAATCAGCGCCCTGGGGGGCCAGAGGGGACGAGGGGAGAGGAC 1658
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Db   1373 CAACACCACCGGCCACAGCGTCACCAATCACAGTCCT-GGCAGGCAAGGAACGACCAGGAGAAAAAGG 1431

Qy   1659 AGAGAAAAAAGAAAAACACAGAGTAGAGAAAGTGAAATAAATGAATAAAACAATAAAATATTT 1716
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Db   1432 AGACGGGGGAGGAGAAAACAGCAATGAGGAACAATCAGTGTCT-GGCAGGCAAGAACGAGAAAG 1489
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                    www-bio.llnl.gov/bbrp/image/image.html
                    Insert Length: 1143   Std Error: 0.00
                    Seq primer: -40UP from Gibco
                    High quality sequence stop: 454.

FEATURES            Location/Qualifiers
     source         1..678
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                    /db_xref="taxon:9606"
                    /clone_lib="NCI_CGAP_Brn25"
                    /clone="IMAGE:2467075"
                    /tissue_type="anaplastic oligodendroglioma"
                    /lab_host="DH10B"
                    /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
                    modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                    strand cDNA was primed with a Not I - oligo(dT) primer [5'
                    TGTTACCAATCTGAACTGGGACGGCGGCCGCAATAGTTTTTTTTTTTTTTTTTT
                    T 3']; double-stranded cDNA was ligated to Eco RI
                    adaptors (Pharmacia), digested with Not I and cloned into
                    the Not I and Eco RI sites of the modified pT7T3 vector.
                    Library is normalized, and was constructed by Bento
                    Soares and M.Fatima Bonaldo."
BASE COUNT          133 a      199 c      161 g      182 t      3 others
ORIGIN

Query Match    35.48%;   Score 672.4;   DB 9;   Length 678;
Best Local Similarity   99.4%;   Pred. No. 2.9e-111;
Matches  673;   Conservative  0;   Mismatches  4;   Indels  0;   Gaps  0;

Qy  1200  TCGAGAGACTCAATGACTTGGGACTTAGACTTAGGGTGGGGCTCGGCCTCGGCCTCTCGAAAAAGTGCTTAAG  1259
          ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   677  TCGAGAGACTCAATGACTGGGACTTAGACTTAGGGTGGGGCTCGGCCTCGGCCTCTCGAAAAGTGCTTAAG   618

Qy  1260  AAAATCTTCTCAGTTCTCCTTGCAGAGGACTCGGCGCGGCGAAGAGAGCAACGGGCGC  1319
          | |||||||||||||||| |||||||||||| ||||||||||||||||||||||||||
Db   617  ANNATCTTCTCAGTTCTCCNTGCAGAGGACTGGGCGCGGCGAAGAGAGCAACGGGCGC   558

Qy  1320  TGCACAAAGCGGGCCGTGTCCGGTGGTTGGAGTGCGCATGCGCATCAGGCGCTTCTCGGTGG  1379
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Db   557  TGCACAAAGCGGGCGCTGTCGGTGGTTGGAGTGCGCATGCGCATCAGGCGCTTCTCGGTGG   498

Qy  1380  TTGGCGGTGCTGCAGCGAACAGCGGCGCGGCGACACACCTGCACGAACACCGGCGAAACTGC  1439
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   497  TTGGCGTGCTGCAGCGAACAGCGGCGCGGCGACACACCTGCACGAACACCGGCGAAACTGC   438

Qy  1440  TGCGGAGGACACCGTGTACAGAGGAGGGGGTTGATGACCGAGCTGAGGTAGAAAAACGTCTCC  1499
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Db   437  TGCGGAGGACACCGTGTACAGAGGAGGCGGGGTTGATGACCGAGCTGAGGTAGAAAAACGTCTCC   378

Qy  1500  GAGAAGGGGAGGAGGAGGAATCATGTTACGCCCCGGGAAGTAGGACACCTCGTCCAGTCGTGCTTGGGT  1559
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Db   377  GAGAAGGGGAGGAGGAGGAATCATGTACGCCCCGGGAAGTAGGACACCTCGTCCAGTCGTGCTTGGGT   318

Qy  1560  TTGGCCCCAGCCCATGATCCTCCGAAATCTGGTTGGGCATCCACATACGGCCCAATGTCACA  1619
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   317  TTGGCCCCAGCCCATGATCCTCCGAAATCTGGTTGGGCATCCACATACGGCCCAATGTCACA   258

Qy  1620  ACAATCAGCCCCTGGGCAGCAGCCAGGAGGAGAGGAAGAAGAAAGAAAAACACAGCA  1679
          |||||||||| ||||||||||||||||| |||||||||||||||||||||||||||
Db   257  ACAATCAGCCCTGGGCAGCAGCCAGGAGAAAGAAAGAAAAACACAGCA   198

Qy  1680  TGAGAACACAGTAAATAAAATGAATAAAACAATAAAAATATTTAGCCCCTCGTTTCGTTTGCTTACT  1739
          |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db   197  TGAGAACACAGTAAATAAAATAAAACAATAAAAATATTTAGCCCCTCGTTTCGTTTGCTTACT   138

Qy  1740  GGCCCAGGAAATGGTACCAAATTTTTTCACGTTTTGGACTTGCACAGCTT  1799
          |||| |||||||||||||||||||||||||| ||||||||||||||||
Db   137  GGCCAGGAAATGGTACCAAATTTTTTCACGTGTTTTGGACTTGCACAGCA   78

Qy  1800  AGAGAGAATTTAACACTGTTTCAAACCCGGGGGAGTTGGCTGTGTTGTTTAAAGAAGAAGACCATT  1859
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    77  AGAGAGAATTTAACACTGTTTCAAACCCGGGGGAGTTGGCTGTGTTGTTTAAAGAAGAAGACCATT   18

Qy  1860  AAATGCTTTAGACAGTG  1876
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Db     1  AAATGCTTTAGACAGTG   1
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RESULT 9
BM547680
LOCUS       BM547680                696 bp    mRNA    linear   EST 20-FEB-2002
DEFINITION  AGENCOURT_6507108 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5727798
            5', mRNA sequence.
ACCESSION   BM547680
VERSION     BM547680.1  GI:18781656
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 696)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Invitrogen
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12722  row: h  column: 07
FEATURES            Location/Qualifiers
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                    /db_xref="taxon:9606"
                    /clone="IMAGE:5727798"
                    /clone_lib="NIH_MGC_124"
                    /tissue_type="hippocampus"
                    /lab_host="DH10B"
                    /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV
                    (destroyed); Site_2: NotI; RNA source male hippocampus,
                    age 27. Library is oligo-dT primed and directionally
                    cloned (EcoRV site is destroyed upon cloning). Average
                    insert size 1.4 kb, insert size range 0.9-4 kb. Library is
                    normalized and enriched for full-length clones and was
                    constructed by C. Gruber (Invitrogen). Research Genetics
                    tracking code 012."
BASE COUNT          188 a      197 c      134 g      197 t      17 others
ORIGIN

Query Match    35.4%;   Score 672.4;   DB 13;   Length 696;
Best Local Similarity   98.7%;   Pred. No. 2.8e-111;
Matches  673;   Conservative  0;   Mismatches  9;   Indels  0;   Gaps  0;

Qy  1210  ATGACTGGGACTTAGACTTAGGGTGGGGCTCGGCCTCGGCCTCTCGAAAAAGTGCTTAAGAAAATCTTCT  1269
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4  ATGACTGGGACTTAGACTTAGGGTGGGGCTCGGCCTCGGCCTCTCGAAAAAGTGCTTAAGAAAATCTTCT   63

Qy  1270  CAGTTCTCCTTGCAGAGGACTGGGCGCGGCGAAGAGAGCAACGGGCGCTGCACAAAGC  1329
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    64  CAGTTCTCCTTGCAGAGGACTGGGCGCGGCGAAGAGAGCAACGGGCGCTGCACAAAGC   123

Qy  1330  GGGCGCTGTCGGTGGTTGGAGTGCGCCATGCGCATCAGGCGCTTCTCGGTGGTTGGCGTGCT  1389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   124  GGGCGCTGTCGGTGGTTGGAGTGCGCCATGCGCATCAGGCGCTTCTCGGTGGTTGGCGTGCT   183

Qy  1390  GCAGCGAACAGCGGCGCGGCGACACCACCTGCACGAACACCGGCGAAACTGCTGCGGAGGACA  1449
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   184  GCAGCGACAGCGGCGCGGCGACACCACCTGCACGAACACCGGCGAAACTGCTGCGGAGGACA   243

Qy  1450  CCGTGTACAGAGCAGGCGGCGGTTGATGACCGAGCTGAGGTAGAAAAACGTCTCCGAGAAGGGGGA  1509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   244  CCGTGTACAGAGCAGGCGGCGGTTGATGACCGAGCTGAGGTAGAAAAACGTCTCCGAGAAGGGGA   303
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RESULT 10
BI917149
BI917149

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Qy  1510 GGAGGATCATGTACGCCCGGAAGTAGGACCTCGTCGTCCAGTCGTCGGTTCGGTTTGGGCCGCAG 1569
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Db   304 GGAGGATCATGTACGCCCGGAAGTAGGACCTCGTCGTCCAGTCGTCTGCTTGGGGTTTGGGCCGCAG 363

Qy  1570 CCATGATCCTTCCGAATCTGGTTGGGCATCCAGCATACGGCCAAATGTCACACAAATCAGCC 1629
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Db   364 CCATGATCCTTCCGAATCTGGTTGGGCATCCAGCATACGGCCAAATGTCACACAAATCAGCC 423

Qy  1630 CTGGGCAGACACGAGCCAGGAGGAGAGACACAGAGACGATGAGAACACA 1689
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Db   424 CTGGGCAGACACGAGCCAGGAGGAGAGACACAGAGACGATGAGAACACA 483

Qy  1690 GTAAATGAATAAAAACCATAAAAATATTTAGCCCCTCTGTTCTGCTTACTGGCCAGGAAA 1749
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Db   484 GTAAATAAATAAAACCATAAAAATATTTAGCCCCTCTGTTCTGCTTACTGGCCAGGAAA 543

Qy  1750 TGGTACCCAATTTTTCAGTGTTGGACTTGACAGCTCTTCTTTTGCCACAAGCAAGAGAAGAATT 1809
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Db   544 TGGTACCCAATTTTTCAGTGTTGGACTTGACAGCTCTTCTTTTGCCACAAGCAAGAGAAGAATT 603

Qy  1810 TAACACTGTTTCAAACCCCGGGGAGTTGGGCTGTGTGTTAAAGAAAGACCCATTAAATGCTTTA 1869
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Db   604 TAACACTGTTTCAAACCCCGGGGAGTTGGGCTGTGTGTTANAGAAAGACCCATTANATGCTTTA 663

Qy  1870 GACAGTGTAAAAAAAAAAAAAAA 1891
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Db   664 GACAGTGTAAAAANNNNNNNNAA 685
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LOCUS   BI917149   747 bp   mRNA   linear   EST 16-OCT-2001
DEFINITION 603181571F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5245648 5',
            mRNA sequence.
ACCESSION   BI917149
VERSION   BI917149.1 GI:16181111
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 747)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LtAM11619 row: n column: 17
            High quality sequence stop: 737.
FEATURES   Location/Qualifiers
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                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks. Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed upon
                     cloning). Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb. Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen). Research Genetics tracking code 017. Note:

RESULT 11
BE271770
BE271770

BASE COUNT   140 a   245 c   216 g   146 t
ORIGIN

Query Match   35.08%; Score 664.2; DB 13; Length 747;
Best Local Similarity 98.6%;
Conservative 0; Mismatches 8; Indels 2; Gaps 2;
Matches 691;   Pred. No. 8.3e-110;

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Db    47 GCCAACTCCGGAGGGCC-GGTGCTGCGGCCCGGGAGCCGGAGGGCGGAGGAGGCAGAGACCCG 105

Qy    61 CAGCCCGGGAGCCCGAGCCGGATGCCAGGTCTCCGGGAGCGGGGCGGGAGGAGCAGAGGACCCG 120
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Db   106 CAGCCCGGGAGCCCGAGCCGGATGCCAGGTCTCCGGGAGCGGGGCGGGAGGAGCAGAGGACCCTA 165

Qy   121 AGCTACGACCGTGCCTGCTCGTCTTCCGGGGCGGGGCCAGCAGCGGGGCCGCACCTCGGGCACAGC 180
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Db   166 AGCTACGACCGTGCCTGCTCGTCTTCCGGGGCGGGGCCAGCAGCGGGGCCGCACCTCGGGCACAGC 225

Qy   181 CGCTGCAGCCGGGGAGCCCTCCGCTGCTGTCGCGGCGCCGGGGCGGGGCCGCTCGGCAGCCCACAGC 240
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Db   226 CGCTGCAGCCGGGGAGCCCTCCGCTGCTGTCGCGGCGCCGGGGCGGGGCCGCTCGGCAGCCCACAGC 285

Qy   241 GCCCCGGGACTCCCGGGAGGAATGTGGGGTCCTAGGCATGCGGCGGAACTTTTTTGCGGATTGTT 300
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Qy   301 CTTGCTTCCAGGCTTTGCGGCTGCAAATCCAGTGCTACCAGTGTGGAAGGAATTCCAGCTGAA 360
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Db   346 CTTGCTTCCAGGCTTTGCGGCTGCAAATCCAGTGCTACCAGTGTGGAAGGAATTCCAGCTGAA 405

Qy   361 CAACGACTGCTCCTCCCCCGGAGTTCATTGTGAATTGCACGGTGAACGTTCAGACATGTG 420
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Db   406 CAACGACTGCTCCTCCCCCGGAGTTCATTGTGAATTGCACGGTGAACGTTCAGACATGTG 465

Qy   421 TCAGAAAAGAAGTGATGGAGCAAAAGTCCCGGGATCATGTACCGACGTCCTTGTGCATCATC 480
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Db   466 TCAGAAAAGAAGTGATGGAGCAAAAGTCCCGGGATCATGTACCGACGTCCTTGTGCATCATC 525

Qy   481 AGCGGCCCTGTCTCATCGCCTCTTCGCGGGTACCAGTGTCCTTCTGCCTCCCAGGGAAAACTGAA 540
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Db   526 AGCGGCCCTGTCTCATCGCCTCTTCGCGGGTACCAGTGTCCTTCTGCCTCCCAGGGAAAACTGAA 585

Qy   541 CTCAGTTTGCATCAGCTGCTGCAACACACCCTCTTTGTTGTAACGGGCCAAGGCCCAAGAAAAG 600
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Db   586 CTCAGTTTGCATCAGCTGCTGCAACACACCCTCTTTGTTGTAACGGGCCAAGGCCCAAGAAAAG 645

Qy   601 GGGAAGTTCTGCCTCCGGCCCCTCAGCCCCACCACCATCCTGTTCCTCAAATTT 660
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Db   646 GGGAAGTTCTGCCTCAGCCCCTCAGCCCCACCACCATCCTGTTCCTCAAATTT 705

Qy   661 AGCCCTCTCTTCTCGGCCAC-ACTGCTGAAGCTGAAGGAGATGC 700
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Db   706 AGCCCTCTCTTCTCGGCCAACAACTGCTGAAGCTGAAGGAGAATGC 746
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LOCUS   BE271770   799 bp   mRNA   linear   EST 26-OCT-2000
DEFINITION 601141674F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3141450 5',
            mRNA sequence.
ACCESSION   BE271770
VERSION   BE271770.1 GI:9145793
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 799)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)

Left result

COMMENT   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM11 row: c column: 19
High quality sequence stop: 721.

FEATURES   Location/Qualifiers
source   1..799
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3141450"
/clone_lib="NIH_MGC_9"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT   171 a   225 c   199 g   204 t
ORIGIN

Query Match 34.7%; Score 658.8; DB 10; Length 799;
Best Local Similarity 96.6%; Pred. No. 7.6e-109;
Matches 767; Conservative 2; Mismatches 14; Indels 11; Gaps 9;

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Qy  494 ATGCGGCCTCTGCCGGGTACCATCCTTCTCTGCTCTCTCGCCCCCAGGGAAAACTGAACTCAGTTTGCATC 553
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Db    1 ATGCGGCCTCTGCCGGGTACCAGTCCTTCTGCTCTCTCCA-GGAACTGAACTCAGTTTGCATC 59

Qy  554 AGCTGCGTGCAACACCCCCTCTTTTGTAACGGGCCAAGGCCCAGAAAAAGGGAAGTTCTGCC 613
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   60 AGCTGCGTGCAACACCCCTCTTTGTAACGGGCCAAGGCCCAGAAAAAGGGAAGTTCTGCC 119

Qy  614 TCGGCCCTCAGGCCAGGCGCTCCGCACCACCACCATCCTCGTTCCTCAAATTAGCCCTCTTCTCG 673
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  120 TCGGCCCTCAGGCCA-GGCTCCGCACCACCACCATCCGTTCCTCAAATTAGCCCTCTTCTCG 178

Qy  674 GCACACTGCTGAAGCTGAAAGAGAGATGCCACC--CCCTCGTGCATTGTTCTTCCAGCCCTC 731
        ||||||||||||||||||||||||||||||||  |||||||||||||||||||||||||||
Db  179 GCACACTGCTGAAGCTGAAGGAGAGATGCCACCCCCCTCGTGCATTGTTCTTCCAGCCCTC 238

Qy  732 GCCCCCAACCCCCAACCTCCCGAGTGTAGTGTCAGTTTCTTCTTCTGGGTAGTCCTTTTATTCTGGGTAG 791
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  239 GCCCCCAACCCCCAACCTCCCGAGTGTGAGTGTCAGTTTCTTCTTCCTGGTGTCCTTTTATTCTGGGTAG 298

Qy  792 GGAGCGGGAGTCCGCGTTGTCTTCTTTGTTGTTCCTGTGCAAATATGAAAAGAGACTCGGTAAAGC 851
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  299 GGAGCGGGAGTCCGTGTTGTCTTCTTTGTTGTCGTGCAAATAATGAAAGAGCTCGGTAAAGC 358

Qy  852 ATTCTGAATAAAATTCAGCYTGACTGAAGATTTTCAGTATGTACTTGAAGGAAGAGAGGTGGAG 911
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Db  359 ATTCTGAATAAAATTCAGCCTGACTGAATTTTCAGTATGTACTTGAAGGAAGAGAGGTGGAG 418

Qy  912 TGAAAGTTCACCCCCAYGTCTCGTGTAACCGGAGTCAAGGCCAGGCTGGCGAGAGTCWGTGCC 971
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Db  419 TGAAAGTTCACCCCCAYGTCTCGTGTAACCGGAGTCAAGGCCAGGCTGGCGAGAGTCC 478

Qy  972 TTAGAAGTTCACTGAGGTGGGCATCGGCTTTTGTAAAGCCTCCCAGTGTCCATTCCATCC 1031
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Db  479 TTAGAAGTCACTGAGGTGGGCAACTGCC-TTTGTAAAGCCTCCCAGTGTCCATTCCATCC 537

Qy 1032 TGATGGGGGCATAGTTTGAGACTGCAGAGTGAGAGTGACGCGTTTTCTTAGGGCTGGAGGGC 1091
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Db  538 TGATGGGGGCATAGTTTGAGACTGCAGAGTGAGAGTGACG-TATCTTAGGGCTGGAGGGC 596
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Right result

RESULT 12
LOCUS   BE385990   676 bp   mRNA   linear   EST   21-JUL-2000
DEFINITION   601276636F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617696 5',
mRNA sequence.
ACCESSION   BE385990
VERSION   BE385990.1   GI:9331355
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 676)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM285 row: g column: 09
High quality sequence stop: 653.

FEATURES   Location/Qualifiers
source   1..676
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3617696"
/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT   168 a   172 c   199 g   137 t
ORIGIN

Query Match 34.7%; Score 657.6; DB 10; Length 676;
Best Local Similarity 99.1%; Pred. No. 1.3e-108;
Matches 672; Conservative 0; Mismatches 4; Indels 0; Gaps 1;

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Db  597 CAGTTCCCACTCAAAGGGTCCCTTCGCTTGACATTCAAATTCATGCCTCCTGAAAAACCATT 656

Qy 1151 CTCTGCAGCAGAATTGGCGTGGTTTTCGCGCCGCCTCCCCCTCAGTTGGGGCTCTAG-TGACTCGAGACTCA 1209
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||
Db  657 CTCTGCAGCAGAATTGGCGTGGTTTTCGCGCCGCCTCCCCCTCAGTTGGGGCTCTAGTTGACTCGAGACTCA 716

Qy 1210 ATGA-CTGGGACTTAGACTGGGGCGTCGGCGCTCGGGCCTCGGCTCTCCTCGAAAGTGCTTAAGAAAATCTTC 1268
        |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  717 ATGACCTGGGACTTAAACTGGGGTCGGCGCTTCG--TCTGAAAGTGCTTAAGACAATCTTC 774

Qy 1269 TCAGTTCTCCTTGC 1282
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Db  775 TCAGTCCTCCTTGC 788
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Right lower sequence block

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Qy 1109 TCCCTCGCCTTGACATTCAAACTTCATGCTCCTGAAAACCAATTCTCTGCAGCAGAATTGGC 1168
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Db    1 TCCCTCGCCTTGACATTCAAACTTCATGCTCCTGAAAACCAATTCTCTGCAGCAGAATTGGC 60

Qy 1169 TGGTTTCGCGCCGCCTGAGTTGGGCTCTAGTTGGTGACTCGAGGACTCAAATGACTGGGACTTAGGACTG 1228
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Db   61 TGGTTTCGCGCCGCCTGAGTTGGGCTCTAGTTGACTCGAGGACTCAAATGACTGGGACTTAGACTG 120
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Qy  1229 GGGCTGCGGCTGCTGCTGCTGAAAAGTGCTTAAGAAAAATCTTCTCAGTTCTCCTTGCAGAGGA 1288
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Db   121 GGGCTGCGGCTGCTGCTGCTGAAAAGTGCTTAAGAAAAATCTTCTCAGTTCTCCTTGCAGAGGA  180

Qy  1289 CTGGCGCGGGACGGCGAAGAGCAACGGGCGCCTGCACAAAGGGCGCCGCTGTCGGTGGTGGA 1348
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Db   181 CTGGCGCGGGACGGCGAAGAGCAACGGGCGCCTGCACAAAGGGCGCCGCTGTCGGTGGTGGA  240

Qy  1349 GTGCGCATGTACCGCGAGCGCGCCTTCTCGTGTGCTGCGCGACGAGCGGCGGCGCCAGCA 1408
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Db   241 GTGCGCATGTACCGCGAGCGCGCCTTCTCGTGTGCTGCGCGACGAGCGGCGGCGCCAGCA  300

Qy  1409 CACCACCTGCACGAACACCCGCCCGAAACTGCTGCGGAGGACACCGTGTACAGGAGCCGGGTT 1468
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Db   301 CACCACCTGCACGAACACCCGCCCGAAACTGCTGCGGAGGACACCGTGTACAGGAGCCGGGTT  360

Qy  1469 GATGACCGGAGCGTGAGGTAGAAAAAAACGTCTCCGAGAAGGGGAGGAGGGATCATGTACGCCCG 1528
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Db   361 GATGACCGGAGCGTGAGGTAGAAAAAAACGTCTCCGAGAAGGGGAGGAGGGATCATGTACGCCCG  420

Qy  1529 GAAGTAGGACCTCGTCCAGTCGTGCTTGGGGTTTGGCCCGCCATGATCCTTCCGGAATCTG 1588
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Db   421 GAAGTAGGACCTCGTCCAGTCGTGCTTGGGGTTTGGCCCGCCATGATCCTTCCGGAATCTG  480

Qy  1589 GTTGGGCATCCAGCATACGGCAGCCAATGTCACACAACAATCAGCCCTGGGCAGACACGAGCAGG 1648
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Db   481 GTTGGGCATCCAGCATACGGCAGCCAATGTCACACAACAATCAGCCCTGGGCAGACACGAGCAGG  540

Qy  1649 AGGGAGAGAGACAGAAAAGAAAACACAGCAGCATGAGAGACAGAAAATGAATAAAAAACCATA 1708
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Db   541 AGGGAGAGAGACAGAAAAGAAAACACAGCAGCATGAGAGACAGTAAATAAATAAAAAACCATA  600

Qy  1709 AAATATTTTAGCCCCTCGTTCTCGTGTGTGCTTACTGGGCCAGGAAATGGTACCAAATTTTTCAGTG 1768
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db   601 AAATATTTTAGCCCCTCGTTCTCTGCTTACTGGGCCGGGAAATGGTCCCA--TTTTCAGTG  658

Qy  1769 TTGGACTTGACAGCTTCT 1786
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Db   659 TTGGACTTGACAGGTTCT  676
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RESULT 13
BI919074
LOCUS       BI919074         704 bp    mRNA      linear   EST 16-OCT-2001
DEFINITION  603180881F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5244956 5',
            mRNA sequence.
ACCESSION   BI919074
VERSION     BI919074.1  GI:16200128
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 704)
  AUTHORS   NIH-MGC http://mgc.ncl.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM1618  row: a  column: 21
            High quality sequence start: 4
            High quality sequence stop: 702.
FEATURES             Location/Qualifiers
     source          1..704
                     /organism="Homo sapiens"
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BASE COUNT      132 a     237 c     204 g     131 t
ORIGIN

Query Match      34.3%;  Score 651.4;  DB 13;  Length 704;
Best Local Similarity  99.7%;
Matches  663;  Conservative  0;  Mismatches  1;  Indels  1;  Gaps  1;
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Qy     1 GCCAAACTCCCGGAGGGGCTCTGGTTGCTCTCCGGCCCCGGGAGCCGCGAGGACGGGAGGCAGAGAGACCCG   60
         |||||||||||||| | ||||| || |||||||||||||||||||||||||||||||||||||||||||||
Db    40 GCCAAACTCCCGGAGGCGC--GGTGCTCTCGGCCCCGGGAGCCGCGAGGACGGGAGGCAGAGAGACCCG   98

Qy    61 CAGCCGGGAGAGCCCGGAGCGGGGGAGATGGCAGGCTTCCCGGAGGCGGCCACCTGGCGGCTCCTCTA  120
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Db    99 CAGCCGGGAGAGCCCGGAGCGGGGGAGATGGCAGGCTTCCCGGAGGCGGCCACCTGGCGGCTCCTCTA  158

Qy   121 AGCTACGACCGTCGTCTCCGGGCACCAGCGCCCCGGCCGGCCTCGGCAGCCCAGCCACAGC  180
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Db   159 AGCTACGACCGTCGTCTCCGGGCACCAGCGCCCCGGCCGGCCTCGGCAGCCCAGCCACAGC  218

Qy   181 CGCTGCAGCGCGGGAGCCTCCGCGTGCGTCGCGCTCCTCTGCAGTGCCGTTGCCCTCCCG  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   219 CGCTGCAGCGCGGGAGCCTCCGCGTGCGTCGCGCTCCTCTGATGCCGTTGCCCTCCCG  278

Qy   241 GCCCCGGGAGCTCCGGGAGGAAATGTGGGTCTCTAGGCATCGCCAACTTTTTTGCGGGATTGTT  300
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Db   279 GCCCCGGGGACTCCGGGAGAAATGTGGGTCTCTAGGCATCGCGAACTTTTTTGCGGGATTGTT  338

Qy   301 CTTGCTTCCAGGGCTTTGCGCTGCAAATCCACTGCTGCAAATTCCAGTGTGAAGAAATTCCAGCTGAA  360
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Db   339 CTTGCTTCCAGGGCTTTGCGCTGCAAATCCACTGCTGCAAATTCCAGTGTGAAGAAATTCCAGCTGAA  398

Qy   361 CAACGACGTCCTCCCCCCGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTG  420
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Db   399 CAACGACGTCCTCCCCCCGAGTTCATTGTGAATTGCACGGTGAACGTTCAAGACATGTG  458

Qy   421 TCAGAAAGAAGTGAATGGAGCAAAGTGCCGGGATCATGTACCGCAAGTCCTGTGCATCATC  480
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Db   459 TCAGAAAGAAGTGAATGGAGCAAAGTGCCGGGATCATGTACCGCAAGTCCTGTGCATCATC  518

Qy   481 AGCGGCCTGTCTCATCGCCTCTGCGGGTACCAGTCCTTCTGCCTCCCAGGGAAAACTGAA  540
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Db   519 AGCGGCCTGTCTCATCGCCTCTGCGGGTACCAGTCCTTCTCCCAGGGAAACTGAA  578

Qy   541 CTCAGTTTGCATCAGCGTGCTGCAACACCCCTCTTTGTAACGGGCCCAAGAGAAAG  600
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Db   579 CTCAGTTTGCATCAGCTGCTGCAACACCCCTCTTTGTAACGGGCCAAGAGAAAG  638

Qy   601 GGGAAGTTCTGCCTCGGCCCTCAGGCCCAGGCGTCCGGCCCACACCCATCCTGGTTCCTCAAAAATT  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   639 GGGAAGTTCTGCCTCGGCCCTCAGGCCCAGGCGTCCGGCCCACCACCATCCTGTTCCTCAAATT  698

Qy   661 AGCCC 665
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Db   699 AGCCC 703
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RESULT 14
AW149665/c
LOCUS       AW149665         690 bp    mRNA      linear   EST 03-NOV-1999
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DEFINITION  xf40h05.x1 NCI_CGAP_Brn50 Homo sapiens cDNA clone IMAGE:2620569 3'
            similar to SW:GP39_HUMAN O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR
            GPR39. ;, mRNA sequence.
ACCESSION   AW149665
VERSION     AW149665.1  GI:6197561
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 690)
  AUTHORS   NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTGAP), Tumor Gene Index
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Burt Feuerstein, M.D., Mark Israel, M.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Possible reversed clone: similarity on wrong strand
            Seq primer: -40UP from Gibco
            High quality sequence stop: 402.
FEATURES             Location/Qualifiers
     source          1..690
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                     /lab_host="DH10B (phage resistant)"
                     /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; 1st strand cDNA was prepared from
                     medulloblastoma tumor tissue, and was then primed with a
                     Not I - oligo(dT) primer. Double-stranded cDNA was ligated
                     to Eco RI adaptors (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of the modified
                     pT7T3 vector. This library is normalized. Library
                     constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT      142 a    196 c    160 g    191 t      1 others
ORIGIN
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Query Match         34.3%;   Score 651.2;  DB 10;   Length 690;
Best Local Similarity 96.5%;  Pred. No. 1.9e-107;
Matches   665;  Conservative   0;  Mismatches  24;  Indels   0;  Gaps   0;
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Qy    1200 TCGAGACTCAATGACTGGGACTTAGACTGGGGCTCGGCCTCTGAAAACGTGCTTAAG 1259
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Db     689 TCGAAATTCAATGACTGGGAATTAGACTTGGGCGCCTTCGTTCTTGAAAAGTGCTTAAG 630
Qy    1260 AAAATCTTCTCAGTTCTCTTCCTTGCCAGAGGACTTGGGCCCCGCGCGGAGGGCCGGGCGC 1319
           || ||||||||||||| || ||||||||||||||||||||||||||||||||||||||||
Db     629 AAAATCTTCTCAGTTCTCTCCCACCAGAGGACTTGGGCCACGCGGAGGCAACGGGCGGCGC 570
Qy    1320 TGCACAAAAGCGGCGGCGCTGTCGGTGGGGGAGTGCGCAATGTAGCCGCAGGCGGTTCTGTGG 1379
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     569 TGCACAAAGCGGCGGCGCTGTCGGTGGTGGAGTGCGCCANGTAGCGCCAGGCGGCTTCTCCGTGG 510
Qy    1380 TTGGCGTGCTGCCAGCGACAGCGGCGCACCACGACCACCTGCACGAAACCCCGCGAAACTGC 1439
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     509 TTGGCGTGCTGCCAGCGACAGCGGCGCACCACGACCACCTGCACGAAACACCCCGCGAAACTGC 450
Qy    1440 TGCGAGGACGACACCGTGTACAGGAGGCGGGGTTGATGACCCGAGCTGAGGTAGAAAAAACGTCTCC 1499
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Db     449 TGCGAGGACACCGTGTACAGGAGGCGGGGGTTGATGACCCGAGCTCAGGTAGAAAAAACGTCTCC 390
Qy    1500 GAGAAGGGGAGGGGAGGGGAGGATCATGTTACGCCCGGAAGTAGGAGACCTCGTCCAGTGTGCTTGGGT 1559
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     389 GAGAAGGGGAGGAGGAGGATCATGTTACGCCCGGAAATCTGGTTGGGCGCATCCACCAATGTCACA 330
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RESULT 15
LOCUS       BI554034        698 bp    mRNA        linear   EST 05-SEP-2001
DEFINITION  603235426F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:5309527
            5', mRNA sequence.
ACCESSION   BI554034
VERSION     BI554034.1  GI:15441348
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 698)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11784  row: d  column: 08
            High quality sequence stop: 687.
FEATURES             Location/Qualifiers
     source          1..698
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5309527"
                     /clone_lib="NCI_CGAP_Brn67"
                     /tissue_type="anaplastic oligodendroglioma with 1p/19q
                     loss"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 2.3 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT      131 a    231 c    204 g    132 t
ORIGIN
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Query Match         34.0%;   Score 645;  DB 13;   Length 698;
Best Local Similarity 98.7%;  Pred. No. 2.4e-106;
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Qy    1620 ACAATCAGCCCTGGGCAGACACGGAGCAGGAGGGGAGGAGAGAAAAGAAAAACACAGCA 1679
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Db     269 ACAATCAGCCCTGGGCAGACACGAGCAGGAGAAGAGAGAGAAGAAAAACACAGCA 210
Qy    1680 TGAGAACACAGTAAATGAATAAAACCATAAAAATATTAGCCCCCTCGTTCTGTGCTTACT 1739
           ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     209 TGAGAACACAGTAAATAAAATAAAACCATAAAAATATTTAGCCCCTCTGTTCTGTGCTTACT 150
Qy    1740 GGCCCAGGAAATGGTACCCAATTTTTTCAGTGTTGGACTTGACAGCTTCTTTTTGCACAAGCA 1799
           ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db     149 GGCCCAGGGAAATGGTACCCAATTTTTTCAGTGTTGGACTTGACAGCTTCTTTTTGCCACAAGCA 90
Qy    1800 AGAGAGAATTTAACACTGTTTCAAACCCGGGGAGTTGGCTGTGTTAAAGAAGACCATT 1859
           ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db      89 AGAGAGAATTTAACACTGTTTCAAACCCGGGGAGTTGGCTGTGTTAAAGAAGACCATT 30
Qy    1860 AAATGCTTTAGACAGTGTAAAAAAAAAAA 1888
           |||||||||||||||||||| |||| |||
Db      29 AAATGCTTTAGACAGTGTATTTATACCAA 1
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Matches   692;  Conservative   0;  Mismatches   5;  Indels   4;  Gaps   4;

Qy     2  CCAACTCCGGAGGCTCTGGTTGCTCTCGGCGCCCGGGAGCGGGAGGAGGCAGAGACCCGC   61
          |||||||||||||| |  ||||||||| ||||||||||||||| |||| ||||||||||||
Db     1  CCAACTCCGGAGGCGC-GGTGCTCGGCCCCGGGAGCGGGAGCCGAGCGGGGAGAGACCCGC   59

Qy    62  AGCCGGGGAGCCCGAGCGGGGCGGAGCCGCGGAGGCTCCCGGCGGCCACCTGGCGGTCCTCTCCTGCTCCTCCTAA  121
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    60  AGCCGGGGAGCCCGAGCGGGGCGGAGCCGCGGAGGCTCCCGGCGGCCACCTGGCGGTCCTCTCCTGCTCCTCCTAA  119

Qy   122  GCTACGACCGTCGTTCTCCGGGCGCCACCAGCCGCGGGGCCCCAGCGCCTTCGGCAGCCCAGCCACCAGCC  181
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   120  GCTACGACCGTCGTTCTCCGGGCGCCACCAGCGCGGGGCCCCAGCGCCTTCGGCAGCCCAGCCACCAGCC  179

Qy   182  GCTGCAGCCGCGGGGCGCAGCCTCCGCTGCTCGTGCGCCTCCCTCTGATGCGCTTGCCCTCTCCCGG  241
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   180  GCTGCAGCCGCGGGGCAGCCTCCGCTGCTCGTGCGCCTCCCTCTGATGCGCTTGCCCTCTCCCGG  239

Qy   242  CCCCGGGGACTCCCGGGAGAAATGTGGGGTTCCTAGGCATGCGGCAAACTTTTTGCGGATTGTTC  301
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   240  CCCCGGGGACTCCCGGGAGAAATGTGGGGTTCCTAGGCATCGCGGCAAACTTTTTGCGGATTGTTC  299

Qy   302  TTGCTTCCAGGCTTTTGCGCGTGCAAAATCCAGTGCTGCTACCAGTGTGAGAGAATTCCAGCTGAAC  361
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   300  TTGCTTCCAGGCTTTTGCGCGTGCAAAATCCAGTGCTACCAGTGTGAAGAGAATTCCAGCTGAAC  359

Qy   362  AACGACTGCTCCTCCCCCCGAGTTCATTGTGAATTGCCACGGTGAACGTTCAAGACATGTGT  421
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   360  AACGACTGCTCCTCCCCCGAGTTCATTGTGAATTGCCACGGTGAACGTTCAAGACATGTGT  419

Qy   422  CAGAAA-GAAGTGATGGAGCAAAAGTGCCGGGATCATGTACCGCAAGTCCGTGCATCATC  480
          ||||||  |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   420  CAGAAACGAAGTGATGGAGCAAAAGTGCCGGGATCAATGTACCGCAAGTCCGTGCATCATC  479

Qy   481  AGGGGCCCTGTCTCATCGCCTCTGCCGGGTACCAGTGCCTTCTTGCTCCCCAGGGAAACTGAA  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   480  AGGGGCCCTGTCTCATCGCCTCTGCCGGGTACCAGTCCTTCTTGCTCCCCAGGGAAACTGAA  539

Qy   541  CTCAGTTTGCATCAGCTGCTGCAACACCCCTCTTTTGTAACGGGCCCAAGGCCCAAGAAAAG  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   540  CTCAGTTTGCATCAGCTGCTGCAACACCCCTCTTTTGTAACGGGCCCAAGGCCCAAGAAAAG  599

Qy   601  GGGAAGTTCTGCCTCGGCCCCTCAGGCCCACAGGCTCCGCACCACCCATCCTGTTCCTCAAATT  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   600  GGGAAGTTCTGCCTCGGCCCCTCAGGCTCCGACCACCACCATCCTGTTCCTCAAATT  659

Qy   661  AGCCCTCTTCTCGGCACACTGCTGAAGCTGAAGGAGATGCC  701
          |||||||||||||||||||||| |||  ||||||||||||
Db   660  AG-CCTCTTCTCGG-ACACTGCTGAAGCTGAGGGAAATTGCC  698

Search completed: November  7, 2002, 15:03:02
Job time : 2553.39 secs
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